


[ExPASy Home page](#)
[Site Map](#)
[Search ExPASy](#)
[Contact us](#)
[Proteomics tools](#)
[Swiss-Prot](#)

Search for

=====

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 9 AA
Date run: 2004-08-04 13:20:52 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,529,856 sequences; 486,583,783 total letters

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr Q8NXX6	Ser-Asp rich fibrinogen-binding bone sialoprotein-bind...	34	0.23
<input type="checkbox"/>	tr Q8NXX5	Ser-Asp rich fibrinogen-binding bone sialoprotein-bind...	34	0.23
<input type="checkbox"/>	tr Q8CQ72	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr Q99W47	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr Q99W46	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr Q932F7	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr Q6GBS5	Putative surface anchored protein [SAS0520] [Staphyloc...	34	0.23
<input type="checkbox"/>	tr Q6GBS4	Bone sialoprotein-binding protein [SAS0521] [Staphyloc...	34	0.23
<input type="checkbox"/>	tr Q7A780	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	34	0.23
<input type="checkbox"/>	tr Q9KI13	Fibrinogen-binding protein SdrG [sdrG] [Staphylococcus...	34	0.23

<input type="checkbox"/>	tr O86489	Sdr E protein [sdr E] [Staphylococcus aureus]	34	0.23
<input type="checkbox"/>	tr O86488	SdrD protein [sdrD] [Staphylococcus aureus]	34	0.23
<input type="checkbox"/>	tr O70022	Fibrinogen-binding protein precursor [Staphylococcus e...	34	0.23
<input type="checkbox"/>	tr Q8NXX7	Ser-Asp rich fibrinogen-binding bone sialoprotein-bind...	32	1.3
<input type="checkbox"/>	tr Q8CMP4	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bind...	32	1.3
<input type="checkbox"/>	tr Q99W48	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	32	1.3
<input type="checkbox"/>	tr Q6GJA7	Putative surface anchored protein [sdrC] [Staphylococc...	32	1.3
<input type="checkbox"/>	tr Q6GBS6	Putative surface anchored protein [SAS0519] [Staphyloc...	32	1.3
<input type="checkbox"/>	tr Q7A781	Ser-Asp rich fibrinogen-binding, bone sialoprotein-bin...	32	1.3
<input type="checkbox"/>	tr Q8KWM1	Surface protein SdrI [Staphylococcus saprophyticus]	32	1.3
<input type="checkbox"/>	tr Q9KI14	Putative cell-surface adhesin SdrF [sdrF] [Staphylococ...	32	1.3
<input type="checkbox"/>	tr O86487	Sdrc protein [sdrc] [Staphylococcus aureus]	32	1.3
<input type="checkbox"/>	tr Q8NXJ1	Fibrinogen-binding protein [clfA] [Staphylococcus aure...	31	1.8
<input type="checkbox"/>	tr Q99VJ4	Fibrinogen-binding protein A, clumping factor [clfA] [...	31	1.8
<input type="checkbox"/>	tr Q932C5	Fibrinogen-binding protein [fnb] [Staphylococcus aureu...	31	1.8
<input type="checkbox"/>	tr Q6GB45	Clumping factor [SAS0752] [Staphylococcus aureus subsp...	31	1.8
<input type="checkbox"/>	tr Q6GJA6	Bone sialoprotein-binding protein [bbp] [Staphylococcu...	30	4.4
<input type="checkbox"/>	tr Q9KWX6	Bone sialoprotein-binding protein [bbp] [Staphylococcu...	30	4.4

Graphical overview of the alignments

to resubmit your query after masking regions matching [PROSITE](#) profiles or Pfam HMMs

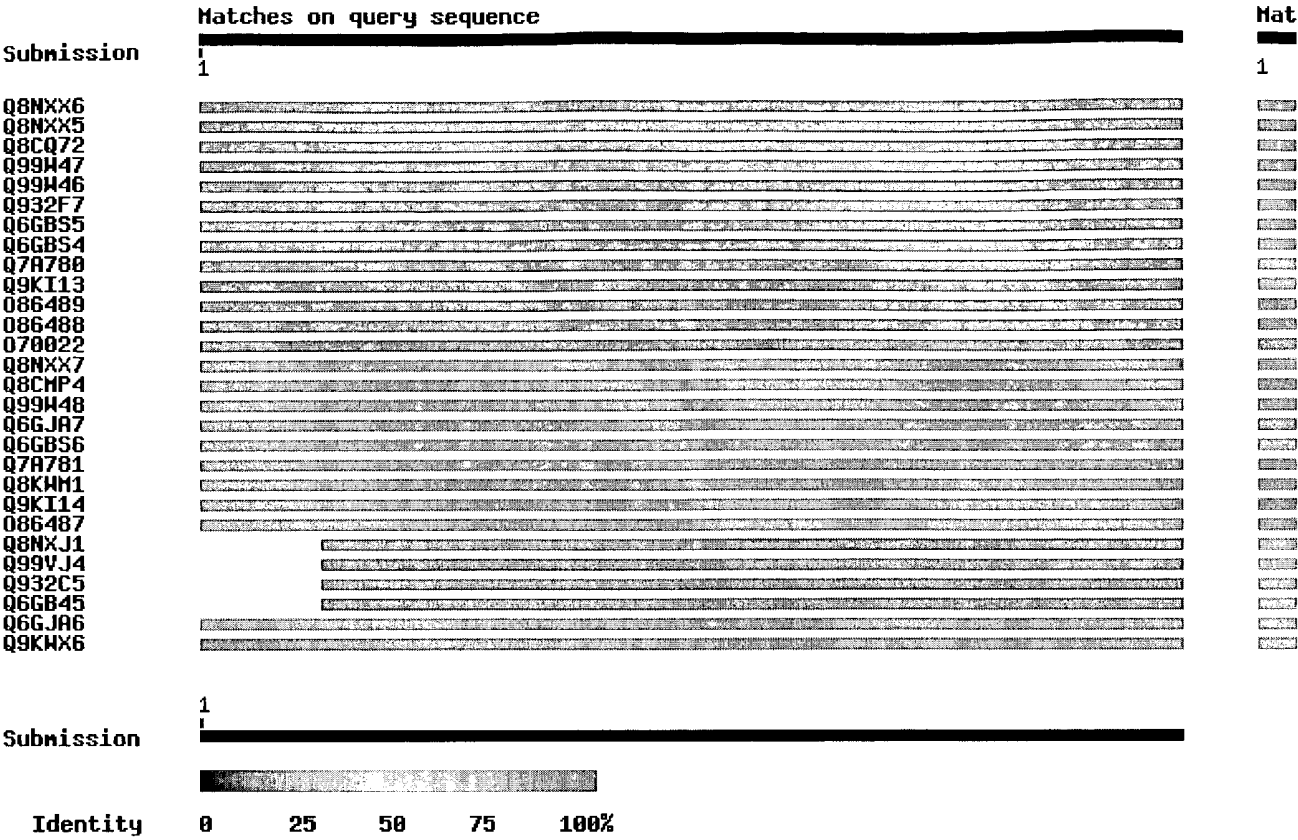
([?](#) Help) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits



Pfam hits





Alignments

tr Q8NXX6 Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein [sdrD] [Staphylococcus aureus (strain MW2)] 1347 AA align

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 339 TYTFTDYVD 347

tr Q8NXX5 Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein [sdrE] [Staphylococcus aureus (strain MW2)] 1141 AA align

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 365 TYTFTDYVD 373

tr Q8CQ72 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1056
protein AA
[SE0331] [Staphylococcus epidermidis ATCC 12228] [align](#)

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 372 TYTFTDYVD 380

tr Q99W47 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1385
protein AA
[sdrD] [Staphylococcus aureus (strain Mu50 / ATCC [align](#)
700699)]

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 339 TYTFTDYVD 347

tr Q99W46 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1141
protein AA
[sdrE] [Staphylococcus aureus (strain N315)] [align](#)

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 365 TYTFTDYVD 373

tr Q932F7 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding** 1141
protein AA
[sdrE] [Staphylococcus aureus (strain Mu50 / ATCC [align](#)
700699)]

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 365 TYTFTDYVD 373

tr Q6GBS5 **Putative surface anchored protein [SAS0520] [Staphylococcus** 1365

aureus
subsp. aureus MSSA476]

AA
[align](#)

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 339 TYTFTDYVD 347

tr [Q6GBS4](#) **Bone sialoprotein-binding protein [SAS0521] [Staphylococcus aureus subsp. aureus MSSA476]**

1141
AA
[align](#)

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 365 TYTFTDYVD 373

tr [Q7A780](#) **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein [sdrD] [Staphylococcus aureus (strain N315)]**

1385
AA
[align](#)

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 339 TYTFTDYVD 347

tr [Q9KI13](#) **Fibrinogen-binding protein SdrG [sdrG] [Staphylococcus epidermidis]**

931
AA
[align](#)

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 370 TYTFTDYVD 378

tr [O86489](#) **Sdr E protein [sdr E] [Staphylococcus aureus]** 1166 AA

[align](#)

Score = 34.1 bits (73), Expect = 0.23

Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 370 TYTFTDYVD 378

tr O86488 **SdrD protein [sdrD] [Staphylococcus aureus]** 1315 AA

align

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 339 TYTFTDYVD 347

tr O70022 **Fibrinogen-binding protein precursor [Staphylococcus epidermidis]**

1092
AA
align

Score = 34.1 bits (73), Expect = 0.23
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 TYTFTDYVD 9
TYTFTDYVD
Sbjct: 372 TYTFTDYVD 380

tr Q8NXX7 **Ser-Asp rich fibrinogen-binding bone sialoprotein-binding protein [sdrC] [Staphylococcus aureus (strain MW2)]**

955
AA
align

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 281 TYTFTNYVD 289

tr Q8CMP4 **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein [SE2395] [Staphylococcus epidermidis]**

1633
AA
align

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9

TYTFT+YVD
Sbjct: 460 TYTFTNYVD 468

tr [Q99W48](#) **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein** 953
[sdrC] [Staphylococcus aureus (strain Mu50 / ATCC 700699)] AA [align](#)

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 281 TYTFTNYVD 289

tr [Q6GJA7](#) **Putative surface anchored protein [sdrC] [Staphylococcus aureus subsp. aureus MRSA252]** 906
AA [align](#)

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 272 TYTFTNYVD 280

tr [Q6GBS6](#) **Putative surface anchored protein [SAS0519] [Staphylococcus aureus subsp. aureus MSSA476]** 957
AA [align](#)

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 281 TYTFTNYVD 289

tr [Q7A781](#) **Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein** 953
[sdrC] [Staphylococcus aureus (strain N315)] AA [align](#)

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 281 TYTFTNYVD 289

tr Q8KWM1 **Surface protein SdrI** [Staphylococcus saprophyticus] 1893 AA

align

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 537 TYTFTNYVD 545

tr Q9KI14 **Putative cell-surface adhesin SdrF** [sdrF] [Staphylococcus epidermidis] 1733 AA

align

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 460 TYTFTNYVD 468

tr Q86487 **Sdrc protein** [sdrc] [Staphylococcus aureus] 947 AA

align

Score = 31.6 bits (67), Expect = 1.3
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 1 TYTFTDYVD 9
TYTFT+YVD
Sbjct: 281 TYTFTNYVD 289

tr Q8NXJ1 **Fibrinogen-binding protein** [clfA] [Staphylococcus aureus (strain MW2)] 946 AA

align

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFPTYVD 9
YTFPTYVD
Sbjct: 316 YTFPTYVD 323

tr Q99VJ4 **Fibrinogen-binding protein A, clumping factor [clfA]** 989 AA
[*Staphylococcus aureus* (strain N315)] align

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFTDYVD 9
YTFTDYVD
Sbjct: 317 YTFTDYVD 324

tr Q932C5 **Fibrinogen-binding protein [fnb]** 935 AA
(strain Mu50 / ATCC 700699)] align

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFTDYVD 9
YTFTDYVD
Sbjct: 317 YTFTDYVD 324

tr Q6GB45 **Clumping factor [SAS0752]** 928 AA
MSSA476] align

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 YTFTDYVD 9
YTFTDYVD
Sbjct: 316 YTFTDYVD 323

tr Q6GJA6 **Bone sialoprotein-binding protein [bbp]** 1137 AA
aureus subsp. *aureus* MRSA252] align

Score = 29.9 bits (63), Expect = 4.4
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 1 TYTFTDYVD 9
TYFTDYVD
Sbjct: 365 TYKFTDYVD 373

tr Q9KWX6 **Bone sialoprotein-binding protein [bbp]** 1171 AA
aureus] align

Score = 29.9 bits (63), Expect = 4.4
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 1 TYTFTDYVD 9
TY FTDYVD
Sbjct: 365 TYKFTDYVD 373

Database: EXPASY/UniProt

Posted date: Jul 29, 2004 5:14 AM
Number of letters in database: 486,583,783
Number of sequences in database: 1,529,856

Lambda	K	H
0.333	0.284	1.87

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of HSP's successfully gapped in prelim test: 0

length of query: 9

length of database: 486,583,783

effective HSP length: 0

effective length of query: 9

effective length of database: 486,583,783

effective search space: 4379254047

effective search space used: 4379254047

T: 16

A: 40

X1: 15 (7.2 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 41 (21.5 bits)

S2: 61 (29.1 bits)

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Proteomics tools](#)[Swiss-Prot](#)

Mark Patent

Mark Range

Mark Section

7

of 83

All Sections

Print

- 8. An isolated antibody that is reactive with the ligand binding A region of the SdrG fibrinogen-binding protein from coagulase-negative Staphylococcus epidermidis.
- 9. A diagnostic kit comprising the antibody according to claim 1 and a means for identifying binding by said antibody.
- 10. Isolated antisera containing the antibody according to claim 1.
- 11. A diagnostic kit comprising antibodies reactive with an SdrG protein from coagulase-negative Staphylococcus epidermidis which is cell-wall associated and which binds both soluble and immobilized fibrinogen.
- 12. A diagnostic kit comprising an antibody reactive with a protein that is cell wall-associated, exhibits cation-dependent ligand-binding and has a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16), wherein the protein is isolated from coagulase-negative Staphylococcus epidermidis.
- 13. An isolated antibody reactive with a protein that is cell wall-associated, exhibits cation-dependent ligand-binding and has a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16), wherein the protein is isolated from coagulase-negative Staphylococcus epidermidis.
- 14. An isolated antibody according to claim 13 wherein the protein comprises the SdrG fibrinogen-binding protein isolated from coagulase-negative Staphylococcus epidermidis.
- 15. An isolated antibody according to claim 13 wherein the protein comprises the ligand binding A region of the SdrG fibrinogen-binding protein isolated from coagulase-negative Staphylococcus epidermidis.

First Hit

Feb 26, 2004

PGPUB-DOCUMENT-NUMBER: 20040038327
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040038327 A1

TITLE: Antibodies to polypeptides from coagulase-negative staphylococci

PUBLICATION-DATE: February 26, 2004

INVENTOR - INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Foster, Timothy J.	Dublin	TX	IE	
McCrea, Kirk	Houston	TX	US	
Hook, Magnus A.O.	Houston	TX	US	
Davis, Stacey	Houston		US	
Ni Eidhin, Deirdre	Dublin		IE	
Hartford, Orla	Meath		IE	

APPL-NO: 10/ 615383 [PALM]
DATE FILED: July 9, 2003

RELATED-US-APPL-DATA:

Application 10/615383 is a division-of US application 09/386962, filed August 31, 1999, US Patent No. 6635473

INT-CL: [07] G01 N 33/554, G01 N 33/569, C07 K 16/12

US-CL-PUBLISHED: 435/7.32; 530/388.4
US-CL-CURRENT: 435/7.32; 530/388.4

REPRESENTATIVE-FIGURES: NONE

ABSTRACT:

Antibodies reactive with isolated proteins, designated SdrF, SdrG and SdrH, and their corresponding amino acid and nucleic acid sequences, are provided which are useful in the prevention and treatment of infection caused by coagulase-negative staphylococcal bacteria such as *S. epidermidis*. The SdrF, SdrG and SdrH proteins are cell-wall associated proteins that specifically bind host proteins and which each have a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16). The antibodies are also useful for the diagnosis and treatment of coagulase-negative staphylococcal infections and may be administered to wounds or used to coat biomaterials to act as blocking agents to prevent or inhibit the binding of coagulase-negative staphylococci to wounds or biomaterials.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a divisional application of U.S. Appln. Ser. No.

09/386,962, filed Aug. 31, 1999, and claims the benefit of U.S. Provisional Applications Serial No. 60/117,119, filed Jan. 25, 1999, and Serial No. 60/098,443, filed Aug. 31, 1998.

Freeform Search

Updated
8/4/2004
VBP

Database:

US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Term:

L2 near10 (antibodies or antisera or
monoclonal or polyclonal or antiserum or mono-
clonal or ig or immune or immunoglobulin)

Display:

50

Documents in Display Format: KWIC

Starting with Number

1

Generate: ☐ Hit List ☒ Hit Count ☐ Side by Side ☐ Image

Search

Clear

Interrupt

Search History

DATE: Wednesday, August 04, 2004 [Printable Copy](#) [Create Case](#)

Set
Name Query

side by
side

Hit
Count Set
Name
result set

DB=USPT; PLUR=YES; OP=AND

L1 mscramm.clm.

0 L1

L2 mscramm

22 L2

L3 L2 near10 (antibodies or antisera or monoclonal or polyclonal or antiserum
or mono-clonal or ig or immune or immunoglobulin)

4 L3

END OF SEARCH HISTORY

WEST Search History

Hide Items Restore Clear Cancel

DATE: Wednesday, August 04, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	clump\$ near3 factor\$	69
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L2	clump\$-near3-factor\$	122
<input type="checkbox"/>	L3	clf or clfa or clf-a	5903
<input type="checkbox"/>	L4	(L3 or l2 or l1) and (staph or staphyloc\$ or aureus! or epidermidis)	122
<input type="checkbox"/>	L5	L4 and (man or woman or homosap\$ or human\$)	96
<input type="checkbox"/>	L6	L5 and (antibod\$ or antiser\$ or anti-ser\$ or ivig or iv-ig or iggiv or igg-iv or immunoglob\$ or globulin)	83
		<i>DB=PGPB; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L7	US-20030099656-A1.did.	1
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L8	(l1 or l6) and (patti or foster or hook).in.	22

END OF SEARCH HISTORY

Inventor search

[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 22 of 22 returned.**

-
- ☐ 1. [20040142348](#). 21 Oct 03. 22 Jul 04. Proteins and polypeptides from coagulase-negative staphylococci. Foster, Timothy J., et al. 435/6; 435/252.3 435/320.1 435/69.1 530/350 536/23.7 C12Q001/68 C07H021/04 C07K014/31.
-
- ☐ 2. [20040141997](#). 21 Oct 03. 22 Jul 04. Methods for treating or preventing infections from coagulase-negative staphylococci. Foster, Timothy J., et al. 424/190.1; 514/44 A61K048/00 A61K039/02.
-
- ☐ 3. [20040101919](#). 15 Sep 03. 27 May 04. Bioinformatic method for identifying surface-anchored proteins from gram-positive bacteria and proteins obtained thereby. Hook, Magnus, et al. 435/7.32; G01N033/554 G01N033/569.
-
- ☐ 4. [20040038327](#). 09 Jul 03. 26 Feb 04. Antibodies to polypeptides from coagulase-negative staphylococci. Foster, Timothy J., et al. 435/7.32; 530/388.4 G01N033/554 G01N033/569 C07K016/12.
-
- ☐ 5. [20040006209](#). 05 Mar 03. 08 Jan 04. Monoclonal and polyclonal antibodies recognizing coagulase-negative staphylococcal proteins. Patti, Joseph M., et al. 530/350; C07K001/00 C07K014/00 C07K017/00.
-
- ☐ 6. [20030099656](#). 28 Jan 02. 29 May 03. Monoclonal antibodies to the ClfA protein and method of use in treating or preventing infections. Patti, Joseph M., et al. 424/165.1; 530/388.3 A61K039/40 C07K016/12.
-
- ☐ 7. [20030044418](#). 13 May 02. 06 Mar 03. Method and compositions for inhibiting thrombin-induced coagulation. Davis, Stacey, et al. 424/184.1; A61K039/00 A61K039/38.
-
- ☐ 8. [20020169288](#). 15 Mar 02. 14 Nov 02. Collagen-binding adhesin from staphylococcus epidermidis and method of use. Hook, Magnus, et al. 530/350; C07K001/00 C07K014/00 C07K017/00.
-
- ☐ 9. [20020159997](#). 07 Mar 02. 31 Oct 02. Staphylococcal immunotherapeutics via donor selection and donor stimulation. Patti, Joseph M., et al. 424/142.1; 530/388.15 A61K039/395 C07K016/40.
-
- ☐ 10. [20020102262](#). 22 Mar 01. 01 Aug 02. Collagen binding protein compositions and methods of use. Hook, Magnus, et al. 424/150.1; 530/388.4 A61K039/40 C07K016/12.
-
- ☐ 11. [6703025](#). 31 Aug 99; 09 Mar 04. Multicomponent vaccines. Patti, Joseph M., et al. 424/243.1; 424/184.1 424/190.1 424/193.1 424/203.1 424/234.1 424/244.1 530/350. A61K039/085.
-
- ☐ 12. [6692739](#). 31 Aug 99; 17 Feb 04. Staphylococcal immunotherapeutics via donor selection and donor stimulation. Patti, Joseph M., et al. 424/130.1; 424/137.1 424/150.1 424/185.1 530/387.1 530/387.5 530/388.2 530/388.4. A61K039/395.
-
- ☐ 13. [6685943](#). 21 Jan 98; 03 Feb 04. Fibronectin binding protein compositions and methods of use. Hook, Magnus, et al. 424/185.1; 424/184.1 424/190.1 514/12 514/13 514/14 514/15. A61K039/00.
-
- ☐ 14. [6680195](#). 25 Nov 98; 20 Jan 04. Extracellular matrix-binding proteins from staphylococcus

aureus. Patti; Joseph M., et al. 435/320.1; 536/23.7. C07H021/04 C12N015/00.

- ☐ 15. 6635473. 31 Aug 99; 21 Oct 03. Polypeptides and polynucleotides from coagulase-negative staphylococci. Foster; Timothy J., et al. 435/320.1; 435/252.3 435/325 536/23.1 536/23.2 536/23.4 536/24.3 536/24.32. C07H021/04 C12N015/11 C12N015/63 C12N001/20.
- ☐ 16. 6288214. 14 May 97; 11 Sep 01. Collagen binding protein compositions and methods of use. Hook; Magnus, et al. 530/387.1; 424/130.1 424/139.1 424/141.1 424/150.1 424/164.1 424/165.1 530/350 530/388.1 530/388.4 530/389.1. C07K016/00 C12P021/08 A61K039/395 A61K039/40.
- ☐ 17. 6177084. 19 Oct 99; 23 Jan 01. S. aureusfibrinogen binding protein. Foster; Timothy James, et al. 424/243.1; 424/184.1 424/185.1 424/190.1 424/200.1 435/243 435/252.3 435/320.1 435/69.1 435/69.3 435/71.1 530/350. A61K039/085.
- ☐ 18. 6008341. 22 Aug 94; 28 Dec 99. S. aureus fibrinogen binding protein gene. Foster; Timothy James, et al. 536/23.7; 435/243 435/252.3 435/320.1 435/69.1 435/69.3 536/23.1. C07H021/04.
- ☐ 19. 5648240. 24 May 94; 15 Jul 97. MHC II analog from Staphylococcus aureus. Hook; Magnus, et al. 435/69.3; 424/185.1 424/243.1 435/252.3 435/320.1 530/300 530/350 530/825 536/23.7. C12N015/31 C07K014/31 A61K039/085.
- ☐ 20. WO 200272600A. New anti- clumping factor A (ClfA) monoclonal antibody, useful for treating or preventing Staphylococcus aureus infection e.g. wound infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in a human or animal. DOMANSKI, P, et al. A61K038/00 A61K039/395 A61K039/40 C07K000/00 C07K016/00 C07K016/12.
- ☐ 21. WO 200064925A. Use of proteins, Clf40 and Clf41, to inhibit the adhesion of leukocytes to fibrinogen. FOSTER, T J, et al. C07K001/00 C07K014/00 C07K017/00.
- ☐ 22. WO 200012132A. Immunizing patients to treat staphylococcal infections comprises administering immunoglobulins having higher antibody titer to staphylococcal adhesin protein. FOSTER, T J, et al. A61K000/00 A61K038/00 A61K039/395 A61P031/04 C07K016/00 C07K016/40 G01N033/569.

Generate Collection

Print

Terms	Documents
(L1 or L6) and (patti or foster or hook).in.	22

Prev Page

Next Page

Go to Doc#

424/165.1; 514/2 A61K039/40 A61K038/16.

☐ 14. [20030211995](#). 20 Dec 02. 13 Nov 03. Methods and formulations for eradicating or alleviating staphylococcal nasal colonization using lysostaphin. Kokai-Kun, John Fitzgerald, et al. 514/12; A61K038/17.

☐ 15. [20030187245](#). 07 Apr 03. 02 Oct 03. Nucleic acid constructs containing hybrid promoters for use in gene therapy. Seifart, Klaus-Heinrich, et al. 536/23.2; 435/455 A61K048/00 C07H021/04 C12N015/85.

☐ 16. [20030171563](#). 13 May 02. 11 Sep 03. Regulators of bacterial virulence factor expression. McNamara, Peter J.. 536/23.1; C07H021/02 C07H021/04.

☐ 17. [20030153020](#). 14 Aug 02. 14 Aug 03. Identification of sortase gene. Schneewind, Olaf, et al. 435/7.32; 435/193 435/252.3 435/320.1 435/6 435/69.3 530/388.26 536/23.2 C12Q001/68 G01N033/554 G01N033/569 C07H021/04 C12N009/10 C12N015/74 C12P021/02 C12N001/21.

☐ 18. [20030105020](#). 18 Nov 02. 05 Jun 03. Use of a composition. Flock, Jan-Ingmar, et al. 514/12; A61K038/17.

☐ 19. [20030104635](#). 02 Jul 02. 05 Jun 03. Screening methods. Jakobsen, Bent Karsten. 436/518; 435/7.9 G01N033/53 G01N033/542 G01N033/543.

☐ 20. [20030099656](#). 28 Jan 02. 29 May 03. Monoclonal antibodies to the ClfA protein and method of use in treating or preventing infections. Patti, Joseph M., et al. 424/165.1; 530/388.3 A61K039/40 C07K016/12.

☐ 21. [20030096432](#). 21 Mar 02. 22 May 03. Screening methods. Jakobsen, Bent Karsten. 436/518; G01N033/543.

☐ 22. [20030096320](#). 01 Oct 02. 22 May 03. Oil bodies and associated proteins as affinity matrices. Moloney, Maurice, et al. 435/7.5; 530/370 530/400 G01N033/53 C07K014/415.

☐ 23. [20030087864](#). 09 Jul 02. 08 May 03. DNA vaccine against staphylococcus aureus. Talbot, Brian, et al. 514/44; A61K048/00.

☐ 24. [20030059910](#). 01 Oct 02. 27 Mar 03. Oil bodies and associated proteins as affinity matrices. Moloney, Maurice, et al. 435/183; 424/192.1 424/193.1 530/413 C12N009/00 A61K039/385 A61K039/00 C07K017/00 C07K016/00 C07K014/00 A23J001/00 C07K001/00.

☐ 25. [20030054436](#). 03 Jan 97. 20 Mar 03. STAPHYLOCOCCUS AUREUS POLYNUCLEOTIDES AND SEQUENCES. KUNSCH, CHARLES A., et al. 435/69.1; 435/252.3 435/320.1 536/23.1 536/23.7 C12P021/02 C12N005/06 C07H021/04 C12N001/21.

☐ 26. [20030054409](#). 25 Jul 02. 20 Mar 03. Novel complex-forming proteins. Jerome, Valerie, et al. 435/7.1; 435/183 435/320.1 435/325 435/69.5 435/69.7 530/350 530/351 G01N033/53 C12P021/02 C12N009/00 C07K014/715 C07K014/52.

☐ 27. [20030044783](#). 09 Mar 01. 06 Mar 03. Human genes and gene expression products. Williams, Lewis T., et al. 435/6; 435/183 435/320.1 435/325 435/69.1 530/350 530/388.1 536/23.2 C12Q001/68 C07H021/04 C12N009/00 C12P021/02 C12N005/06 C07K014/435 C07K016/40.

-
- ☐ 28. 20030044418. 13 May 02. 06 Mar 03. Method and compositions for inhibiting thrombin-induced coagulation. Davis, Stacey, et al. 424/184.1; A61K039/00 A61K039/38.
-
- ☐ 29. 20030022178. 21 Aug 01. 30 Jan 03. Identification of sortase gene. Schneewind, Olaf, et al. 435/6; 435/110 435/193 435/252.3 435/32 435/34 435/7.32 C12Q001/68 G01N033/554 G01N033/569 C12Q001/18 C12Q001/04 C12N009/10 C12N001/21.
-
- ☐ 30. 20030008398. 14 Jun 02. 09 Jan 03. Self-enhancing, pharmacologically controllable expression systems. Mueller, Rolf, et al. 435/455; 435/320.1 536/23.2 C12N015/85 C07H021/04.
-
- ☐ 31. 20020173462. 27 Aug 01. 21 Nov 02. Fibrinogen binding protein. Boden Wastfelt, Maria K., et al. 514/12; 435/235.1 435/252.33 435/320.1 435/69.1 530/350 536/23.7 A61K038/17 C07H021/04 C12N007/00 C12P021/02 C12N001/21 C12N015/74.
-
- ☐ 32. 20020169288. 15 Mar 02. 14 Nov 02. Collagen-binding adhesin from *staphylococcus epidermidis* and method of use. Hook, Magnus, et al. 530/350; C07K001/00 C07K014/00 C07K017/00.
-
- ☐ 33. 20020159997. 07 Mar 02. 31 Oct 02. *Staphylococcal* immunotherapeutics via donor selection and donor stimulation. Patti, Joseph M., et al. 424/142.1; 530/388.15 A61K039/395 C07K016/40.
-
- ☐ 34. 20020151049. 04 Apr 02. 17 Oct 02. Self-enhancing, pharmacologically controllable expression systems. Mueller, Rolf, et al. 435/320.1; 514/44 A61K048/00 C12N015/00.
-
- ☐ 35. 20020137699. 14 Jul 99. 26 Sep 02. EXPRESSION SYSTEMS COMPRISING CHIMERIC PROMOTERS WITH BINDING SITES FOR RECOMBINANT TRANSCRIPTION FACTORS. MUELLER, ROLF, et al. 514/44; 435/320.1 435/455 536/23.1 536/23.2 800/21 A61K048/00 C12N015/87 C07H021/04.
-
- ☐ 36. 20020129397. 11 Dec 01. 12 Sep 02. Transgenic mice containing brain-specific membrane-anchored protein gene disruptions. Allen, Keith D.. 800/18; 435/320.1 435/354 A01K067/027 C12N005/06 C12N015/00.
-
- ☐ 37. 20020120116. 04 May 98. 29 Aug 02. ENTEROCOCCUS FAECALIS POLYNUCLEOTIDES AND POLYPEPTIDES. KUNSCH, CHARLES A., et al. 536/23.2; 435/252.3 435/320.1 435/69.1 435/70.1 435/71.1 530/350 530/387.9 800/13 C07K016/00.
-
- ☐ 38. 20020102262. 22 Mar 01. 01 Aug 02. Collagen binding protein compositions and methods of use. Hook, Magnus, et al. 424/150.1; 530/388.4 A61K039/40 C07K016/12.
-
- ☐ 39. 20020098166. 21 Jul 98. 25 Jul 02. GENETICALLY MODIFIED CELLS AND THEIR USE IN THE PROPHYLAXIS OR THERAPY OF DISORDERS. HAVEMANN, KLAUS, et al. 424/93.1; 435/325 A61K048/00 C12N005/06.
-
- ☐ 40. 20020081665. 31 Jan 01. 27 Jun 02. Bryostatins, bryopyrans and polyketides: compositions and methods. Haygood, Margo, et al. 435/76; 435/252.3 435/6 514/27 514/28 536/23.2 536/7.1 C12Q001/68 C07H017/08 C07H021/04 C12P019/62 C12N001/21.
-
- ☐ 41. 20020032323. 30 Oct 97. 14 Mar 02. STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES. KUNSCH, CHARLES A., et al. 536/23.7; 435/252.3 435/320.1 435/69.1 536/24.32 C12P021/02 C07H021/04 C12N001/21 C12N015/74.
-

- ☐ 42. [20010046685](#). 28 Jun 01. 29 Nov 01. Control for methods for determining platelet count and platelet function. Moskowitz, Keith A., et al. 435/7.21; G01N033/567.
- ☐ 43. [6759518](#). 09 Apr 99; 06 Jul 04. Single-chain multiple antigen-binding molecule, its preparation and use. Kontermann; Roland, et al. 530/387.3; 435/320.1 530/387.7 536/23.1. C07K016/00 C12P021/08 A61K048/00 C12N015/63.
- ☐ 44. [6737248](#). 03 Jan 97; 18 May 04. *Staphylococcus aureus* polynucleotides and sequences. Kunsch; Charles A., et al. 435/69.1; 435/252.3 435/320.1 536/23.1 536/23.7. C12P021/02.
- ☐ 45. [6733758](#). 01 Apr 99; 11 May 04. Fibrinogen binding protein originating from coagulase-negative *staphylococcus*. Guss; Bengt, et al. 424/243.1; 424/184.1 424/190.1 424/192.1 424/234.1 424/237.1 514/2 530/300 530/350 530/825. A61K030/085 A61K039/02 A61K039/00 C07K001/00.
- ☐ 46. [6703025](#). 31 Aug 99; 09 Mar 04. Multicomponent vaccines. Patti; Joseph M., et al. 424/243.1; 424/184.1 424/190.1 424/193.1 424/203.1 424/234.1 424/244.1 530/350. A61K039/085.
- ☐ 47. [6692739](#). 31 Aug 99; 17 Feb 04. *Staphylococcal* immunotherapeutics via donor selection and donor stimulation. Patti; Joseph M., et al. 424/130.1; 424/137.1 424/150.1 424/185.1 530/387.1 530/387.5 530/388.2 530/388.4. A61K039/395.
- ☐ 48. [6685943](#). 21 Jan 98; 03 Feb 04. Fibronectin binding protein compositions and methods of use. Hook; Magnus, et al. 424/185.1; 424/184.1 424/190.1 514/12 514/13 514/14 514/15. A61K039/00.
- ☐ 49. [6680195](#). 25 Nov 98; 20 Jan 04. Extracellular matrix-binding proteins from *staphylococcus aureus*. Patti; Joseph M., et al. 435/320.1; 536/23.7. C07H021/04 C12N015/00.
- ☐ 50. [6660842](#). 19 Sep 00; 09 Dec 03. Ligand/receptor specificity exchangers that redirect antibodies to receptors on a pathogen. Sallberg; Matti. 530/350; 435/7.1 530/324 530/325 530/326 530/331 530/382 530/807. C07K001/00.

[Generate Collection](#)[Print](#)

Terms	Documents
L5 and (antibod\$ or antiser\$ or anti-ser\$ or ivig or iv-ig or iggiv or igg-iv or immunoglob\$ or globulin)	83

[Prev Page](#)[Next Page](#)[Go to Doc#](#)

[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 50 of 83 returned.**

-
- ☐ 1. [20040142348](#). 21 Oct 03. 22 Jul 04. Proteins and polypeptides from coagulase-negative *staphylococci*. Foster, Timothy J., et al. 435/6; 435/252.3 435/320.1 435/69.1 530/350 536/23.7 C12Q001/68 C07H021/04 C07K014/31.
-
- ☐ 2. [20040141997](#). 21 Oct 03. 22 Jul 04. Methods for treating or preventing infections from coagulase-negative *staphylococci*. Foster, Timothy J., et al. 424/190.1; 514/44 A61K048/00 A61K039/02.
-
- ☐ 3. [20040101919](#). 15 Sep 03. 27 May 04. Bioinformatic method for identifying surface-anchored proteins from gram-positive bacteria and proteins obtained thereby. Hook, Magnus, et al. 435/7.32; G01N033/554 G01N033/569.
-
- ☐ 4. [20040091856](#). 01 Dec 00. 13 May 04. DNA sequences from *staphylococcus aureus* bacteriophage 44AHJD that encode anti-microbial polypeptides. Pelletier, Jerry, et al. 435/6; 435/5 C12Q001/68 C12Q001/70.
-
- ☐ 5. [20040067544](#). 27 Jun 03. 08 Apr 04. Use of adhesion molecules as bond stress-enhanced nanoscale binding switches. Vogel, Viola, et al. 435/7.32; C12Q001/68 G01N033/554 G01N033/569.
-
- ☐ 6. [20040043037](#). 27 Dec 02. 04 Mar 04. *Staphylococcus aureus* polynucleotides and sequences. Kunsch, Charles A., et al. 424/190.1; 435/252.3 435/320.1 435/69.3 530/350 536/23.7 A61K039/02 C07H021/04 C12P021/02 C12N001/21 C07K014/31.
-
- ☐ 7. [20040038327](#). 09 Jul 03. 26 Feb 04. Antibodies to polypeptides from coagulase-negative *staphylococci*. Foster, Timothy J., et al. 435/7.32; 530/388.4 G01N033/554 G01N033/569 C07K016/12.
-
- ☐ 8. [20040033607](#). 01 May 03. 19 Feb 04. Plant vernalization independence (VIP) genes, proteins, and methods of use. Van Nocker, Steven R., et al. 435/468; 435/320.1 435/419 435/69.1 530/350 536/23.6 800/278 C12N015/82 C12N005/10 C07K014/00 C12N015/63 C12N015/29 C12N015/64 A01H005/00 C07H021/04 C12N015/09 C12N015/00.
-
- ☐ 9. [20040029118](#). 03 Jun 02. 12 Feb 04. *Streptococcus pneumoniae* polynucleotides and sequences. Kunsch, Charles A., et al. 435/6; 702/20 C12Q001/68 G06F019/00 G01N033/48 G01N033/50.
-
- ☐ 10. [20040019189](#). 27 Jun 03. 29 Jan 04. Ligand/receptor specificity exchangers that redirect antibodies to receptors on a pathogen. Sallberg, Matti. 530/395; C07K014/31.
-
- ☐ 11. [20040006209](#). 05 Mar 03. 08 Jan 04. Monoclonal and polyclonal antibodies recognizing coagulase-negative *staphylococcal* proteins. Patti, Joseph M., et al. 530/350; C07K001/00 C07K014/00 C07K017/00.
-
- ☐ 12. [20030225251](#). 21 Feb 03. 04 Dec 03. Specificity exchangers that redirect antibodies to a pathogen. Sallberg, Matti, et al. 530/350; C07K014/705 C07K014/195.
-
- ☐ 13. [20030224000](#). 20 Dec 02. 04 Dec 03. Methods for blocking or alleviating *staphylococcal* nasal colonization by intranasal application of monoclonal antibodies. Kokai-Kun, John Fitzgerald, et al.


[ExPASy Home page](#)
[Site Map](#)
[Search ExPASy](#)
[Contact us](#)
[Proteomics tools](#)
[Swiss-Prot](#)

Search for

=====

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
 If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402 (1997).

=====

Query length: 689 AA (of which 3% low-complexity regions filtered out)

Date run: 2004-08-04 12:46:51 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,529,856 sequences; 486,583,783 total letters

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db AC	Description	Score	E-value
<input type="checkbox"/> tr Q6GFB8	MHC class II analog [SAR2030] [Staphylococcus aureus s...	1290	0.0
<input type="checkbox"/> tr Q9Z4P5	MapN protein precursor [mapN] [Staphylococcus aureus]	1287	0.0
<input type="checkbox"/> tr Q53599	MHC class II analog [Staphylococcus aureus]	1229	0.0
<input type="checkbox"/> tr Q9S2Z4	Cell surface protein map-w precursor [map-w] [Staphylo...	979	0.0
<input type="checkbox"/> tr O07318	Outer surface binding 70kD protein (Fragment) [Staphyl...	918	0.0
<input type="checkbox"/> tr Q9K4S8	Map-ND2C protein precursor [map-ND2C] [Staphylococcus ...	910	0.0
<input type="checkbox"/> tr Q8NVR4	Truncated cell surface protein map-w [truncated map-W]...	881	0.0
<input type="checkbox"/> tr Q9XAS5	Map-7 protein precursor [map-7] [Staphylococcus aureus]	835	0.0
<input type="checkbox"/> tr Q9Z4J2	Map protein (Fragment) [map] [Staphylococcus aureus]	824	0.0
<input type="checkbox"/> tr Q99QS1	Truncated map-w protein [SAV1938] [Staphylococcus aure...	727	0.0

<input type="checkbox"/>	sp	P21223	OMP7_STAAU 70 kDa outer membrane protein precursor (Fr...	208	2e-52
<input type="checkbox"/>	tr	Q99QS2	Truncated map-w protein [SAV1937] [Staphylococcus aure...	147	6e-34
<input type="checkbox"/>	tr	Q8NVR5	Truncated map-w protein [truncated map-W] [Staphylococ...	140	8e-32
<input type="checkbox"/>	tr	Q99VA9	Hypothetical protein [SAV0981] [Staphylococcus aureus ...	115	2e-24
<input type="checkbox"/>	tr	Q7A6G0	SA0841 protein [SA0841] [Staphylococcus aureus (strain...	115	2e-24
<input type="checkbox"/>	tr	Q6GIA6	Putative exported protein [SAR0944] [Staphylococcus au...	115	3e-24
<input type="checkbox"/>	tr	Q8NXE3	MW0863 protein [MW0863] [Staphylococcus aureus (strain...	114	8e-24
<input type="checkbox"/>	tr	Q6GAU5	Putative exported protein [SAS0851] [Staphylococcus au...	114	8e-24
<input type="checkbox"/>	tr	Q6GEM4	Putative exported protein [SAR2295] [Staphylococcus au...	84	8e-15
<input type="checkbox"/>	tr	Q99S64	Hypothetical protein [SAV2205] [Staphylococcus aureus ...	83	1e-14
<input type="checkbox"/>	tr	Q6G7B0	Putative exported protein [SAS2104] [Staphylococcus au...	83	1e-14
<input type="checkbox"/>	tr	Q7A483	SA2006 protein [SA2006] [Staphylococcus aureus (strain...	83	1e-14
<input type="checkbox"/>	tr	Q7A090	MW2130 protein [MW2130] [Staphylococcus aureus (strain...	83	1e-14
<input type="checkbox"/>	tr	Q8G961	Hypothetical protein ORF9 [ORF9] [Staphylococcus aureus]	83	1e-14
<input type="checkbox"/>	tr	Q7RJV0	CCAAT-box DNA binding protein subunit B, putative (Fra...	54	7e-06
<input type="checkbox"/>	tr	Q6LFF0	Hypothetical protein [MAL6P1.307] [Plasmodium falcipar...	54	9e-06
<input type="checkbox"/>	tr	Q8RI19	Hemolysin [FN1817] [Fusobacterium nucleatum (subsp. nu...	53	2e-05
<input type="checkbox"/>	tr	Q8RGZ3	Hemolysin [FN0132] [Fusobacterium nucleatum (subsp. nu...	53	2e-05
<input type="checkbox"/>	tr	Q8I581	Hypothetical protein [PFL1645w] [Plasmodium falciparum...	53	2e-05
<input type="checkbox"/>	tr	Q7RAS6	Hypothetical protein (Fragment) [PY06423] [Plasmodium ...	50	1e-04
<input type="checkbox"/>	tr	Q8RGK2	Hemolysin [FN0291] [Fusobacterium nucleatum (subsp. nu...	50	2e-04
<input type="checkbox"/>	tr	Q8IIG1	Hypothetical protein [PF11_0213] [Plasmodium falciparu...	49	4e-04
<input type="checkbox"/>	tr	Q7RRC0	Hypothetical protein [PY00811] [Plasmodium yoelii yoelii]	49	4e-04
<input type="checkbox"/>	tr	Q8KRR1	Hemolysin [Fusobacterium nucleatum]	48	5e-04
<input type="checkbox"/>	tr	Q7P6S5	Hemolysin [FNV1407] [Fusobacterium nucleatum subsp. vi...	48	7e-04
<input type="checkbox"/>	tr	Q7P5V6	Hemolysin [FNV1203] [Fusobacterium nucleatum subsp. vi...	48	7e-04
<input type="checkbox"/>	tr	Q8IJQ6	Initiation factor 2 subunit family, putative [PF10_013...	47	0.001
<input type="checkbox"/>	tr	Q8IJM3	Hypothetical protein [PF10_0171] [Plasmodium falciparu...	47	0.001
<input type="checkbox"/>	tr	Q7RS53	Hypothetical protein [PY00512] [Plasmodium yoelii yoelii]	47	0.001
<input type="checkbox"/>	tr	Q7RK24	Hypothetical protein [PY03080] [Plasmodium yoelii yoelii]	47	0.001
<input type="checkbox"/>	tr	Q99WH4	Exotoxin 13 [set13] [Staphylococcus aureus (strain Mu5...	47	0.002
<input type="checkbox"/>	tr	Q7A7H2	Exotoxin 13 [set13] [Staphylococcus aureus (strain N315)]	47	0.002
<input type="checkbox"/>	tr	Q8ILS9	Hypothetical protein [PF14_0165] [Plasmodium falciparu...	47	0.002
<input type="checkbox"/>	tr	Q7RR45	Hypothetical protein [PY00892] [Plasmodium yoelii yoelii]	47	0.002
<input type="checkbox"/>	tr	Q97TE6	Hypothetical protein CAP0158 [CAP0158] [Clostridium ac...	46	0.003
<input type="checkbox"/>	tr	Q9RN33	Exotoxin 1 [set1] [Staphylococcus aureus]	46	0.003
<input type="checkbox"/>	tr	Q9RN32	Exotoxin 1 [set1] [Staphylococcus aureus]	45	0.003
<input type="checkbox"/>	tr	Q8IL30	Hypothetical protein [PF14_0419] [Plasmodium falciparu...	45	0.003
<input type="checkbox"/>	tr	Q7RNU0	Hypothetical protein [PY01725] [Plasmodium yoelii yoelii]	45	0.003
<input type="checkbox"/>	tr	Q8IL12	Hypothetical protein [PF14_0438] [Plasmodium falciparu...	45	0.004
<input type="checkbox"/>	tr	Q8NY46	Set24 protein [set24] [Staphylococcus aureus (strain M...	45	0.006
<input type="checkbox"/>	tr	Q6GC56	Exotoxin 5 [SAS0392] [Staphylococcus aureus subsp. aur...	45	0.006
<input type="checkbox"/>	tr	Q8IJA2	Hypothetical protein [PF10_0296] [Plasmodium falciparu...	45	0.006
<input type="checkbox"/>	tr	Q7RR36	Methlytransferase, UbiE/COQ5 family [PY00901] [Plasmod...	45	0.006
<input type="checkbox"/>	tr	Q8I3J8	Hypothetical protein [PFE1330c] [Plasmodium falciparum...	44	0.007

<input type="checkbox"/>	tr	Q8I2A4	Hypothetical protein PFA0180w [PFA0180w] [Plasmodium f...	44	0.007
<input type="checkbox"/>	tr	Q7RM00	Similar to sentrin/SUMO-specific protease [PY02388] [P...	44	0.007
<input type="checkbox"/>	tr	Q8JKP9	Stress-induced protein STI1 [orf62] [Heliothis zea vir...	44	0.010
<input type="checkbox"/>	tr	Q8NY48	Set22 protein [set22] [Staphylococcus aureus (strain M...	44	0.010
<input type="checkbox"/>	tr	Q9ZHL0	Large supernatant protein 2 [lspA2] [Haemophilus ducreyi]	44	0.010
<input type="checkbox"/>	tr	Q6GC58	Exotoxin 1 [SAS0390] [Staphylococcus aureus subsp. aur...	44	0.010
<input type="checkbox"/>	tr	Q7BY44	Large supernatant protein 2 [lspA2] [Haemophilus ducre...	44	0.010
<input type="checkbox"/>	tr	Q6LFM5	Hypothetical protein [MAL6P1.44] [Plasmodium falciparu...	44	0.010
<input type="checkbox"/>	tr	Q8IHV8	Hypothetical protein [PF11_0418] [Plasmodium falciparu...	44	0.010
<input type="checkbox"/>	tr	Q7REY3	235 kDa rhoptry protein (Fragment) [PY04930] [Plasmodi...	44	0.010
<input type="checkbox"/>	tr	Q97277	Kinesin, putative [MAL3P7.1] [Plasmodium falciparum (i...	44	0.010
<input type="checkbox"/>	tr	Q9PQ08	Hypothetical protein UU482 [UU482] [Ureaplasma parvum ...	44	0.013
<input type="checkbox"/>	tr	Q7RKX6	Synthetic antigen of P.falciparum, putative (Fragment)...	44	0.013
<input type="checkbox"/>	tr	Q7RDD8	Hypothetical protein [PY05484] [Plasmodium yoelii yoelii]	44	0.013
<input type="checkbox"/>	tr	Q6GJP2	Exotoxin 1 [set1] [Staphylococcus aureus subsp. aureus...	43	0.017
<input type="checkbox"/>	tr	Q9ZFS5	Exotoxin 1 [set1] [Staphylococcus aureus]	43	0.017
<input type="checkbox"/>	tr	Q8ID19	Hypothetical protein PF13_0360 [PF13_0360] [Plasmodium...	43	0.017
<input type="checkbox"/>	tr	Q7RH89	Asparagine-rich protein [PY04100] [Plasmodium yoelii y...	43	0.017
<input type="checkbox"/>	tr	Q7RFK8	NLI interacting factor, putative [PY04698] [Plasmodium...	43	0.017
<input type="checkbox"/>	tr	Q8IC44	Starp antigen [PF07_0006] [Plasmodium falciparum (isol...	43	0.022
<input type="checkbox"/>	tr	Q8I5Q0	Hypothetical protein [PFL0755c] [Plasmodium falciparum...	43	0.022
<input type="checkbox"/>	tr	Q7R9P1	Hypothetical protein (Fragment) [PY06820] [Plasmodium ...	43	0.022
<input type="checkbox"/>	sp	P38537	SLAP_BACSH Surface-layer 125 kDa protein precursor [Ba...	42	0.028
<input type="checkbox"/>	sp	P55746	CGA2_HELPHY Cytotoxicity associated immunodominant anti...	42	0.028
<input type="checkbox"/>	tr	Q7RIU9	Hypothetical protein (Fragment) [PY03517] [Plasmodium ...	42	0.028
<input type="checkbox"/>	tr	Q9BJY0	235 kDa rhoptry protein (Fragment) [IIIa.1] [Plasmodiu...	42	0.028
<input type="checkbox"/>	tr	Q898L8	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4....	42	0.037
<input type="checkbox"/>	tr	Q7XVF0	OSJNBa0083D01.8 protein [OSJNBa0083D01.8] [Oryza sativ...	42	0.037
<input type="checkbox"/>	tr	Q8IKG8	Rhoptry protein, putative [PF14_0637] [Plasmodium falc...	42	0.037
<input type="checkbox"/>	tr	Q8IHP9	Hypothetical protein [PF11_0480] [Plasmodium falciparu...	42	0.037
<input type="checkbox"/>	tr	Q8I469	Hypothetical protein [PFE0155w] [Plasmodium falciparum...	42	0.037
<input type="checkbox"/>	tr	Q7YXS0	MB2 (Fragment) [Plasmodium gallinaceum]	42	0.037
<input type="checkbox"/>	tr	Q7RRK2	Protein kinase domain, putative [PY00717] [Plasmodium ...	42	0.037
<input type="checkbox"/>	tr	Q7RND4	Chloroquine resistance marker protein (Fragment) [PY01...	42	0.037
<input type="checkbox"/>	sp	Q7TUA3	FMT_PROMP Methionyl-tRNA formyltransferase (EC 2.1.2.9...	42	0.048
<input type="checkbox"/>	tr	Q841F4	Iron-regulated outer membrane protein (Fragment) [fetA...	42	0.048
<input type="checkbox"/>	tr	Q8IL70	Hypothetical protein [PF14_0379] [Plasmodium falciparu...	42	0.048
<input type="checkbox"/>	tr	Q8IL35	Hypothetical protein [PF14_0414] [Plasmodium falciparu...	42	0.048
<input type="checkbox"/>	tr	Q8I437	Hypothetical protein [PFE0320w] [Plasmodium falciparum...	42	0.048
<input type="checkbox"/>	tr	Q7RJT3	Kinesin-like protein K6 [PY03174] [Plasmodium yoelii y...	42	0.048
<input type="checkbox"/>	tr	Q6H1A0	Adhesin (Fragment) [hmw2A] [Haemophilus influenzae]	41	0.063
<input type="checkbox"/>	tr	Q841B7	Iron-regulated outer membrane protein (Fragment) [fetA...	41	0.063
<input type="checkbox"/>	tr	Q8IIV3	Hypothetical protein [PF11_0060] [Plasmodium falciparu...	41	0.063
<input type="checkbox"/>	tr	Q8IHX8	Hypothetical protein [PF11_0398] [Plasmodium falciparu...	41	0.063
<input type="checkbox"/>	tr	Q8IEH7	Hypothetical protein PF13_0079 [PF13_0079] [Plasmodium...	41	0.063

Graphical overview of the alignments[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)

Profile hits**Pfam hits**

Submission	Matches on query sequence					Mat
	1				500	
Q6GF88						
Q9Z4P5						
Q53599						
Q952Z4						
Q07318						
Q9K458						
Q8NVR4						
Q9XAS5						
Q9Z4J2						
Q99Q51						
OMP7_STAAU						
Q99Q52						
Q8NVR5						
Q99V89						
Q7A6G0						
Q6GIA6						
Q8NXC3						
Q6GAU5						
Q6GEM4						
Q99S64						
Q6G7B0						
Q7A483						
Q7A090						
Q8G961						
Q7RJV0						
Q6LFF0						
Q8RI19						
Q8RGZ3						
Q8I581						
Q7RAS6						
Q8RGK2						
Q8IIG1						
Q7RRC0						
Q8KRR1						
Q7P6S5						
Q7P5V6						
Q8IJQ6						
Q8IJH3						
Q7RS53						
Q7RK24						
Q99MH4						
Q7A7H2						
Q8ILS9						
Q7RR45						
Q97TE6						
Q9RN33						
Q9RN32						
Q8IL30						
Q7RNU0						
Q8IL12						
Q8NY46						
Q6GC56						
Q8IJA2						
Q7RR36						
Q8I3J8						
Q8I2A4						
Q7RH00						
Q8JKP9						
Q8NY48						
Q9ZHL0						
Q6GC58						
Q7BY44						
Q6LFH5						
Q8IHV8						
Q7REY3						
Q97277						
Q9PQ08						
Q7RKX6						
Q7RDD8						
Q6GJP2						
Q9ZFS5						
Q8ID19						
Q7RH09						
Q7RFK8						
Q8IC44						
Q8I5Q0						
Q7R9P1						
SLAP_BACSH						
CGA2_HELPY						
Q7RIU9						
Q9BJY8						
Q898L8						
Q7XVF0						
Q8IKG8						
Q8IHP9						
Q8I469						

Alignments

tr Q6GFB8 MHC class II analog [SAR2030] [Staphylococcus aureus subsp. aureus
MRSA252] 689
AA
align

Score = 1290 bits (3337), Expect = 0.0
Identities = 668/689 (96%), Positives = 668/689 (96%)

Query: 1 MKFKSLITTTALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60
MKFKSLITTTALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT
Sbjct: 1 MKFKSLITTTALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60

Query: 61 SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120
SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV
Sbjct: 61 SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120

Query: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTF 180
DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTF
Sbjct: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVPYTITVNGTSQNILSNLTF 180

Query: 181 KKNQQISYKDLNENKSVLKSNGRITDIDLRLSKQAKFTVNFKNGTKKVIDLKAGIYTAN 240
KKNQQISYKDLNENKSVLKSNGRITDIDLRLSKQAKFTVNFKNGTKKVIDLKAGIYTAN
Sbjct: 181 KKNQQISYKDLNENKSVLKSNGRITDIDLRLSKQAKFTVNFKNGTKKVIDLKAGIYTAN 240

Query: 241 LINTGDIKNININVTETKKQAKDKAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300
LINTGDIKNININVTETKKQAKDKAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN
Sbjct: 241 LINTGDIKNININVTETKKQAKDKAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300

Query: 301 LTAKVKSVLKSDRGVSRDLKHAKKAYTTFYFKNGGKRVIHLSNIYTANLVHAKDIKKI 360
LTAKVKSVLKSDRGVSRDLKHAKKAYTTFYFKNGGKRVIHLSNIYTANLVHAKDIKKI
Sbjct: 301 LTAKVKSVLKSDRGVSRDLKHAKKAYTTFYFKNGGKRVIHLSNIYTANLVHAKDIKKI 360

Query: 361 EVTVKTGSKANAERYVPYTIAVNGTSTPNLSDLKFKGDSRVSYSIDITKKVKSVLKYDRGI 420
EVTVKTGSKANAERYVPYTIAVNGTSTPNLSDLKFKGDSRVSYSIDITKKVKSVLKYDRGI
Sbjct: 361 EVTVKTGSKANAERYVPYTIAVNGTSTPNLSDLKFKGDSRVSYSIDITKKVKSVLKYDRGI 420

Query: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFXXXXXXXXXXXXTGSKAKADSY 480
GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLF TGSKAKADSY
Sbjct: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFVKDIKKIDVDVKTGSKAKADSY 480

Query: 481 VPYTIAVNGTSTPIASKLKLNSKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV 540
VPYTIAVNGTSTPIASKLKLNSKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV
Sbjct: 481 VPYTIAVNGTSTPIASKLKLNSKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV 540

Query: 541 HFKNGKTQVVDLKSDFTRNLFVXXXXXXXXXXVKQHTKSNKALNKVSNIATKVKFPVTI 600
HFKNGKTQVVDLKSDFTRNLFV VKQHTKSNKALNKVSNIATKVKFPVTI
Sbjct: 541 HFKNGKTQVVDLKSDFTRNLFVVKDIKKIDVDVKTGSKAKADSY 600

Query: 601 NGFSNVVSNEFAFLHPHKITTDNLAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660
NGFSNVVSNEFAFLHPHKITTDNLAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS
Sbjct: 601 NGFSNVVSNEFAFLHPHKITTDNLAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660

Query: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689
KFVDLKAQKQDSKVFKATDIKKVDIEIKF
Sbjct: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689

tr Q9Z4P5 MapN protein precursor [mapN] [Staphylococcus aureus] 689 AA
align

Score = 1287 bits (3331), Expect = 0.0
Identities = 666/689 (96%), Positives = 668/689 (96%)

Query: 1 MKFKSLITTTLALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60
MKFKSLITTTLALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT
Sbjct: 1 MKFKSLITTTLALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60

Query: 61 SQNILSSLTFNKNQQISYKDIENTKVSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120
SQNILSSLTFNKNQQISYKDIENTKVSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV
Sbjct: 61 SQNILSSLTFNKNQQISYKDIENTKVSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120

Query: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDEAKANVQVPYTITVNGTSQNILSNLTF 180
DLKAGIHTADLINTSDIKAISVNVDTKKQVKDEAKANVQVPYTITVNGTSQNILSNLTF
Sbjct: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDEAKANVQVPYTITVNGTSQNILSNLTF 180

Query: 181 KKNQQISYKDLNENVKSVLKSNRGITDVDLRLSKQAKFTVNFKNGTCKVIDLKAGIYTAN 240
KKNQQISYKDLNENVKSVLKSNRGITDVDLRLSKQAKFTVNFKNGTCKVIDLKAGIYTAN
Sbjct: 181 KKNQQISYKDLNENVKSVLKSNRGITDVDLRLSKQAKFTVNFKNGTCKVIDLKAGIYTAN 240

Query: 241 LINTGDIKNININIVETKKQAKDKEAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300
LINTGDIKNININIVETKKQAKDKEAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN
Sbjct: 241 LINTGDIKNININIVETKKQAKDKEAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300

Query: 301 LTAKVKSVLKSDRGVSEKDLKHAKKAYTVYFKNNGKRVIHLSNIYTANLVHAKDIKKI 360
LTAKVKSVLKSDRGVSEKDLKHAKKAYTVYFKNNGKRVIHLSNIYTANLVHAKDIKKI
Sbjct: 301 LTAKVKSVLKSDRGVSEKDLKHAKKAYTVYFKNNGKRVIHLSNIYTANLVHAKDIKKI 360

Query: 361 EVTVKTGSKANAERYVPYTI AVNGTSTPNLSDLKFKGDSRVSYSDITKKVKSVLKYDRGI 420
EVTVKTGSKANAERYVPYTI AVNGTSTPNLSDLKFKGDSRVSYSDITKKVKSVLKYDRGI
Sbjct: 361 EVTVKTGSKANAERYVPYTI AVNGTSTPNLSDLKFKGDSRVSYSDITKKVKSVLKYDRGI 420

Query: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFXXXXXXXXXXXXX TGSKAKADSY 480
GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLF TGSKAKADSY
Sbjct: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFVKDIDVDVKTGSKAKADSY 480

Query: 481 VPYTI AVNGTSTPIASKLKL SNKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV 540
VPYTI AVNGTSTPIASKL+LSNKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV
Sbjct: 481 VPYTI AVNGTSTPIASKLRLSNKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV 540

Query: 541 HFKNGKTQVVDLKS DIFTRNLFSVXXXXXXXXXXVKQHTKSNKALNKVSN IATKVKFPVTI 600
HFKNGKTQVVDLKS DIFTRNLFSV VKQHTKSNKALNKV+NIATKVKFPVTI
Sbjct: 541 HFKNGKTQVVDLKS DIFTRNLFSVKDIDVDVKTGHTKSNKALNKVANIATKVKFPVTI 600

Query: 601 NGFSNVVSNEFAFLHPHKIT TNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660
NGFSNVVSNEFAFLHPHKIT TNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS
Sbjct: 601 NGFSNVVSNEFAFLHPHKIT TNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660

Query: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689
KFVDLKAQKQDSKVFKATDIKKVDIEIKF
Sbjct: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689

tr Q53599 MHC class II analog [Staphylococcus aureus] 689 AA
align

Score = 1229 bits (3179), Expect = 0.0
Identities = 635/689 (92%), Positives = 648/689 (93%)

Query: 1 MKFKSLITTTTALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60
MKFKSLITTTTALGV+ASTGAN +TNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT
Sbjct: 1 MKFKSLITTTTALGVIASTGANLDTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60

Query: 61 SQNILSSLTFNKNQQISYKDIENKVKSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120
SQNILSSLTFNKNQQISYKDIENKVKSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV
Sbjct: 61 SQNILSSLTFNKNQQISYKDIENKVKSPLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120

Query: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKANVQVPYTITVNGTSQNILSNLTF 180
DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKANVQVPYTITVNGTSQNILSNLTF
Sbjct: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKANVQVPYTITVNGTSQNILSNLTF 180

Query: 181 KKNQQISYKDLNENKSVLKSNGITDIDLRLSKQAKFTVNFNGTKKVIDLKAGIYTAN 240
KKNQQISYKDLNENKSVLKSNGITDIDLRLSKQAKFTVNFNGTKKVIDLKAGIYTAN
Sbjct: 181 KKNQQISYKDLNENKSVLKSNGITDIDLRLSKQAKFTVNFNGTKKVIDLKAGIYTAN 240

Query: 241 LINTGDIKNININIVETKKQAKDKEAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300
LINTG IKNININIVETKKQAKDKEAK NNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN
Sbjct: 241 LINTGGIKNININIVETKKQAKDKEAKVNNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300

Query: 301 LTAKVKSVLKSDRGVSRDLKHAKKAYYTVYFKNGGKRVIHLSNIIYTANLVHAKDIKKI 360
LT KVKSVLKSDRGVSRDLKHAKKAYYTVYFKNGGKRVIHLSNIIYTANLVHAKD+K+I
Sbjct: 301 LTTKVKSVLKSDRGVSRDLKHAKKAYYTVYFKNGGKRVIHLSNIIYTANLVHAKDVKRI 360

Query: 361 EVTVKTGSKANAERYVPYTIAVNGTSTPNLSDLKFKGDSRVSYSDITKKVKSVLKYDRGI 420
EVTVKT SK AERYVPYTIAVNG S P LSDLKF GDSRVSYSDI KVKSVLK+DRGI
Sbjct: 361 EVTVKTGSKVKAERYVPYTIAVNGASNPTLSDLKFTGDSRVSYSDIKKKVKSVLKHDRGI 420

Query: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFXXXXXXXXXXXXTGSKAKADSY 480
GERELKYA+KATYTVHFKNGTKKVINLNS ISQLNLL+ TG+KAK SY
Sbjct: 421 GERELKYAEKATYTVHFKNGTKKVINLNSNISQLNLLYVKDIKNIDIDVKTGAKAKVYSY 480

Query: 481 VPYTIAVNGTSTPIASKLKLSENKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTV 540
VPYTIAVNGT+TPIASKLKLSENKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYT+
Sbjct: 481 VPYTIAVNGTTTPIASKLKLSENKQLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTI 540

Query: 541 HFKNGKTQVVDLKSDFTRNLFSVXXXXXXXXXXVKQHTKSNKALNKVSNIATKVKFPVTI 600
HFKNGKTQVVDLKSDFTRNLFSV VKQ +KSNKALNKV+N ATKVKFPVTI
Sbjct: 541 HFKNGKTQVVDLKSDFTRNLFSVKDIKKIDINVKQQSKSNKALNKVTNKATKVKFPVTI 600

Query: 601 NGFSNVVSNEFAFLHPHKITTNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660
NGFSN+VSNEFAFLHPHKITTNDLNAKLRLAL SDQGITKHDIGLSERTVYKVYFKDGSS
Sbjct: 601 NGFSNLVSNEFAFLHPHKITTNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660

Query: 661 KFVDLKAQKQDSKVFKATDIKKVDIEIKF 689
K DLKAQKQDSKVFKATDIKKVDIEIKF
Sbjct: 661 KLEDLKAQKQDSKVFKATDIKKVDIEIKF 689

tr Q9S2Z4 Cell surface protein map-w precursor [map-w] [Staphylococcus 687 AA

aureus]

align

Score = 979 bits (2530), Expect = 0.0

Identities = 510/688 (74%), Positives = 580/688 (84%), Gaps = 10/688 (1%)

Query: 1 MKFKSLITTTLALGVLASTGANFNTNEASAAAKQIDKSSSSLHHGYSKIQIPYTITVNGT 60
 MKFKSLITTTLALGV+ASTGANFNTNEASAAAK +DKSSS+LHHG+S IQIPYTITVNGT
 Sbjct: 1 MKFKSLITTTLALGVIASTGANFNTNEASAAAKPLDKSSSTLHHGHSNIQIPYTITVNGT 60

Query: 61 SQNILSSLTFNKNQQISYKDIENTKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVV 120
 SQNILSSLTFNKNQ ISYKDIENTKVKSVLYFNRGISDIDLRLSKQA+YTVHFKNGTKRV+
 Sbjct: 61 SQNILSSLTFNKNQNISYKDIENTKVKSVLYFNRGISDIDLRLSKQAEYTVHFKNGTKRVI 120

Query: 121 DLKAGIHTADLINTSDIKAISVNVDTKKQVKDKKEAKANVQVPYTITVNGTSQNILSNLTF 180
 DLK+GI+TADLINTSDIKAISVNVDTKKQ KDK AKANVQVPYTITVNGTSQNILSNLTF
 Sbjct: 121 DLKSGIYTADLINTSDIKAISVNVDTKKQPKDK-AKANVQVPYTITVNGTSQNILSNLTF 179

Query: 181 KKNQQISYKDLENNVKS SVLKS NRGITD VDLRLSKQAKFTVNFKNGT KKVIDLKAGIYTAN 240
 KNQ ISYKDLE+ VKSVL+SNRGITD VDLRLSKQAK+TVNFKNGT KKVIDLKAGIYTAN
 Sbjct: 180 NKNQNISYKDLEDKVKSVLESNRGITD VDLRLSKQAKYTVNFKNGT KKVIDLKAGIYTAN 239

Query: 241 LINTGDIKNININVETKKQAKDKKEAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKN 300
 LIN+ DIK+ININV+TKK ++K AK N QVPYSINLNGT+TNI SNL+FSNKPWTNYKN
 Sbjct: 240 LINSSDIKSININVDTKKHIEKN-AKRNYQVPYSINLNGTSTNILSNLSFSNKPWTNYKN 298

Query: 301 LTAKVKS SVLKS DRGVSE RDLKHAKAYYTVYFKNGGKRVIHLNSNIYTANLVHAKDIKKI 360
 LT+++KSVLK DRG+SE+DLK+AKKAYYTVYFKNGGKR++ LNS YTANLVH KD+K+I
 Sbjct: 299 LTSQIKSVLKHDRGISEQDLKYAKKAYYTVYFKNGGKRILQLNSKNYTANLVHV KDV KRI 358

Query: 361 EVTVKTGSKANAERYVPYTI AVNGTSTPNLS DLKFKGDSRVSYSDITKKVKS SVLK YDRGI 420
 E+TVKTG+KA A+RYVPYTI AVNGTSTP LSDLKF GD RV Y DITKKVKS SVLK+DRGI
 Sbjct: 359 EITVKTGTKAKADRYVPYTI AVNGTSTPILSDLKFTGDP RVGYKDITKKVKS SVLKHDRGI 418

Query: 421 GERELKYAKKATYTVHFKNGTKKVINLNSKISQLNLLFXXXXXXXXXXXXTGS KAKADSY 480
 GERELKYAKKATYTVHFKNG KKVINLNSKISQLNLL+ TGS KAKADSY
 Sbjct: 419 GERELKYAKKATYTVHFKNGKKKVINLNSKISQLNLLYVQDIKKIDIDVKTGS KAKADSY 478

Query: 481 VPYTI AVNGTSTPIASKLKL SNKQLIGYQDLNKKVKS SVLKHDRGINDIELKFAKQAKYTV 540
 VPYTI AVNGTSTPI SKLK+SNKQLI Y+ LN KVKSVLK++RGI+D++LKF AKQAKYTV
 Sbjct: 479 VPYTI AVNGTSTPILSKLKISNKQLISYKYLN DKVKS SVLKNERGISDLDLKFAKQAKYTV 538

Query: 541 HFKNGKTQVVDLKS DIFTRNLFSVXXXXXXXXXXVKQHTKSNKALNKVSNIATKV KFPVTI 600
 +FKNGK QVV+LKSDIFT NLFS VK +K + + V + + +
 Sbjct: 539 YFKNGKKQVNLKSDIFT PNLFSAKDIKKIDIDVKTGSK-----AKADSYVPYTI AV 590

Query: 601 NGFSNVVSNEFAFLHPHKIT TNDLNAKLRLALASDQGITKHDIGLSERTVYKVYFKDGSS 660
 NG S + ++ + I+ LN K++ L S++GI+ D+ +++ Y VYFK+G
 Sbjct: 591 NGTSTPILSKLKISNKQLISYKYLN DKVKS SVLKSERGISDLDLKFAKQAKYTVYFKNGKK 650

Query: 661 KFVDLKA AKQDSKVFKATDIKKVDIEIK 688
 + V+LK+ +F A DIKK+DI++K
 Sbjct: 651 QVNLKSDIFT PNLFSAKDIKKIDIDVK 678

Score = 652 bits (1681), Expect = 0.0

Identities = 340/559 (60%), Positives = 426/559 (75%), Gaps = 6/559 (1%)

Query: 24 NTNEASAAAKQIDKSSSSSLHHGYSKIQIPYTITVNGTSQNILSSSLTFNKNQQISYKDIE 83
NT++ A + +D + +Q+PYTITVNGTSQNILS+LTFNKNQ ISYKD+E+
Sbjct: 133 NTSDIKAISVNVDTKKQPKDKAKANVQVPYTITVNGTSQNILSNLTFNKNQNI SYKDLED 192

Query: 84 KVKSPLYFNRGISDIDLRLSKQAKYTVHFKNCTKRVVDLKGAIHTADLINTSDIKAISVN 143
KVKSVL NRGID+DLRLSKQAKYTV+FKNGTK+V+DLKAGI+TA+LIN+SDIK+I++N
Sbjct: 193 KVKSVLNNGITDIDLRLSKQAKYTVNFKNGTKKVIDLKGAIYTANLINSSDIKSININ 252

Query: 144 VDTKKQVKDKEAKANVQVPYTITVNGTSQNILSNLTFKKNQQISYKDLENNVKSVLKSNR 203
VDTKK +++K AK N QVPY+I +NGTS NILSNL+F +YK+L + +KSVLK +R
Sbjct: 253 VDTKKHIENK-AKRNYQVPYSINLNGTSTNLSNLSFSPKWTNYKNLTSQIKSVLKHDR 311

Query: 204 GITDIDLRLSKQAKFTVNFKNGTKKVIDLKGAIYTANLINTGDIKNININVETKKQAKDK 263
GI++ DL+ +K+A +TV FKNG K+++ L + YTANL++ D+K I I V+T
Sbjct: 312 GISEQDLKYAKKAYYTVYFKNGGKRILQLNSKNYTANLVHVKDVKRIEITVKT-----GT 366

Query: 264 EAKANNQVPYSINLNGTTTNIQSNLAFSNKPWTNYKNLTAKVKSVLKSDRGVSEKDLKHA 323
+AKA+ VPY+I +NGT+T I S+L F+ P YK++T KVKSVLK DRG+ ER+LK+A
Sbjct: 367 KAKADRYVPYTIANGTSTPILSDLKFTGDPVGVYKDITKKVKSVLKHDRGIGERELKYA 426

Query: 324 KKAYYTVYFKNGGKRVIHLSNIYTANLVHAKDIKKIEVTVKTGSKANAERYVPYTIAVN 383
KKA YTV+FKNG K+VI+LNS I NL++ +DIKKI++ VKTGSKA A+ YVPYTIAVN
Sbjct: 427 KKATYTVHFKNKKVINLSKISQLNLLYVQDIKKIDIDVKTGSKAKADSYVPYTIAVN 486

Query: 384 GTSTPNLSDLKFKGDSRVSYSIDITKKVKSVLKYDRGIGERELKYAKKATYTVHFKNCTK 443
GTSTP LS LK +SY + KVKSVLK +RGI + +LK+AK+A YTV+FKNG K+
Sbjct: 487 GTSTPILSKLISNKQLISYKYLNDKVKSVLKNERGISDLDLKFAKQAKYTVYFKNGKKQ 546

Query: 444 VINLSKISQLNLLFXXXXXXXXXXXXTGSKAKADSYVPYTIANGTSTPIASKLKLSNK 503
V+NL S I NL TGSKAKADSYVPYTIANGTSTPI SKLK+SNK
Sbjct: 547 VVNLKSDIFTNLFSAKDIKKIDIDVKTGSKAKADSYVPYTIANGTSTPILSKLKISNK 606

Query: 504 QLIGYQDLNKKVKSVLKHDRGINDIELKFAKQAKYTVHFKNCTQVVDLKSDFTRNLFS 563
QLI Y+ LN KVKSVLK +RGI+D++LKFAKQAKYTV+FKNGK QVV+LKSDIFT NLFS
Sbjct: 607 QLISYKYLNDKVKSVLKSERGISDLDLKFAKQAKYTVYFKNGKKQVVNLKSDIFTNLF 666

Query: 564 VXXXXXXXXXVKQHTKSNK 582
VKQ+TKS K
Sbjct: 667 AKDIKKIDIDVKQYTKSKK 685


Score = 318 bits (814), Expect = 3e-85
Identities = 175/323 (54%), Positives = 229/323 (70%), Gaps = 12/323 (3%)

Query: 51 IPYTITVNGTSQNILSSSLTFNKNQQISYKDIEKVKSVLYFNRGISDIDLRLSKQAKYTV 110
+PYTI VNGTS ILS L F + ++ YKDI KVKSVL +RGI + +L+ +K+A YTV
Sbjct: 374 VPYTIANGTSTPILSDLKFTGDPVGVYKDITKKVKSVLKHDRGIGERELKYAKKATYTV 433

Query: 111 HFKNGTKRVVDLKGAIHTADLINTSDIKAISVNVDTKKQVKDKEAKANVQVPYTITVNGT 170
HFKNG K+V++L + I +L+ DIK I ++V T +AKA+ VPYTI VNGT
Sbjct: 434 HFKNGKKVINLSKISQLNLLYVQDIKKIDIDVKT-----GSKAKADSYVPYTIANGT 488

Query: 171 SQNILSNLTFKKNQQISYKDLENNVKSVLKSNRGITDIDLRLSKQAKFTVNFKNGTKKVI 230
S ILS L Q ISYK L + VKSVLK+ RGI+D+DL+ +KQAK+TV FKNG K+V+
Sbjct: 489 STPILSKLKISNKQLISYKYLNDKVKSVLKNERGISDLDLKFAKQAKYTVYFKNGKKQVV 548

Query: 231 DLKAGIYTANLINTGDIKNININVETKKQAKDKEAKANNQVPYSINLNGTTTNIQSNLAF 290
+LK+ I+T NL + DIK I+I+V+T +AKA++ VPY+I +NGT+T I S L

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Search <input type="text" value="Swiss-Prot/TrEMBL"/>		for <input type="text" value="mhc staphylococcus"/>	<input type="button" value="Go"/>	<input type="button" value="Clear"/>

NiceProt View of TrEMBL: Q9Z4P5

[Printer-friendly view](#)[Request update](#)[Quick BlastP search](#)

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name	Q9Z4P5
Primary accession number	Q9Z4P5
Secondary accession numbers	None
Entered in TrEMBL in	Release 10, May 1999
Sequence was last modified in	Release 10, May 1999
Annotations were last modified in	Release 26, March 2004
Name and origin of the protein	
Protein name	MapN protein [Precursor]
Synonyms	None
Gene name	Name: mapN
From	<i>Staphylococcus aureus</i> [TaxID: 1280]
Taxonomy	Bacteria; Firmicutes; Bacillales; <i>Staphylococcus</i> .

MHC II
homolog

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=Newman;
Hussain S.M., Herrmann M., Heilmann C., Peters G.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references


EMBL	AJ132841; CAA10802.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR005298 ; MAP. Graphical view of domain structure .
Pfam	PF03642 ; MAP; 6. Pfam graphical view of domain structure .
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q9Z4P5 .
PRESAGE	Q9Z4P5 .

ModBase [Q9Z4P5](#).
SMR [Q9Z4P5](#); CF88802B4F47C9CD.
SWISS-2DPAGE [Get region on 2D PAGE](#).
UniRef [View cluster of proteins with at least 50% / 90% identity](#).

Keywords

Signal.

Features



Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	30	30	Potential.
CHAIN	31	689	659	MapN protein.

Sequence information

Length: **689 AA** [This is the length of the unprocessed precursor]

Molecular weight: **76860 Da** [This is the MW of the unprocessed precursor]

CRC64: **CF88802B4F47C9CD** [This is a checksum on the sequence]

10	20	30	40	50	60
MKFKSLITTT	LALGVLASTG	ANFNTNEASA	AAKQIDKSSS	SLHHGYSKIQ	IPYTITVNGT
70	80	90	100	110	120
SQNILSSLTF	NKNQQISYKD	IENKVKSPLY	FNRGISDIDL	RLSKQAKYTV	HFKNGTKRNV
130	140	150	160	170	180
DLKAGIHTAD	LINTSDIKAI	SVNVDTKKQV	KDKEAKANVQ	VPYTITVNGT	SQNILSNLTF
190	200	210	220	230	240
KKNQQISYKD	LENNVKSVLK	SNRGITDVDL	RLSKQAKFTV	NFKNGTKKVI	DLKAGIYTAN
250	260	270	280	290	300
LINTGDIKNI	NINVETKKQA	KDKEAKANNO	VPYSINLNGT	TTNIQSNLAF	SNKPWTNYKN
310	320	330	340	350	360
LTAKVKSVLK	SDRGVSEEDL	KHAKKAYYTV	YFKNGGKRV	HLNSNIYTAN	LVHAKDIKKI
370	380	390	400	410	420
EVTVKTGSKA	NAERYVPYTI	AVNGTSTPNL	SDLKFKGDSR	VSYSBITKKV	KSVLKYDRGI
430	440	450	460	470	480
GERELKYAKK	ATYTVHFKNG	TKKVINLNSK	ISQLNLLFVK	DIKKIDVDVK	TGSKAKADSY
490	500	510	520	530	540
VPYTIAVNGT	STPIASKLRL	SNKQLIGYQD	LNKKVKSVLK	HDRGINDIEL	KFAKQAKYTV

```

550      560      570      580      590      600
|       |       |       |       |       |
HFKNQGTQVV DLKSDIFTRN LFSVKDIKKI DIDVKQHTKS NKALNKVANI ATKVKFPVTI

610      620      630      640      650      660
|       |       |       |       |       |
NGFSNVVSNE FAFLEPHKIT TNDLNAKLRL ALASDQGITK HDIGLSERTV YKVYFKDGSS

670      680
|       |
KFVDLKAQKQ DSKVFKATDI KKVDIEIKF
```

[Q9Z4P5 in FASTA format](#)

[View entry in original TrEMBL format](#)

[View entry in raw text format \(no links\)](#)

[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)




Sequence analysis tools: [ProtParam](#), [ProtScale](#),
[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet \(Java\)](#)




[ScanProsite](#), [MotifScan](#)



Search the [SWISS-MODEL Repository](#)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot				
Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Canada	China	Korea	Switzerland	Taiwan

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
--	-----------------	----------------------	-------------------	-------------------

Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Canada	China	Korea	Switzerland	Taiwan
-------------------	---------------	-----------	---------	--------	-------	-------	-------------	--------

Search for

Search in Swiss-Prot and TrEMBL for: mhcii

Swiss-Prot Release 44.2 of 30-Jul-2004

TrEMBL Release 27.2 of 30-Jul-2004

-
- Number of sequences found in Swiss-Prot₍₀₎ and TrEMBL₍₇₎: **7**
 - Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
 - For more directed searches, you can use the Sequence Retrieval System SRS.
-

Search in Swiss-Prot: There are matches to 0 out of 155596 entries

Search in TrEMBL: There are matches to 7 out of 1365262 entries

Q7ZYW1

SI:dZ194E12.12 (Novel MHCII beta chain protein) (Fragment) {GENE:Name=SI:dZ194E12.12} - Brachydanio rerio (Zebrafish) (Danio rerio)

Q7ZYW2

SI:dZ194E12.11 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ194E12.11} - Brachydanio rerio (Zebrafish) (Danio rerio)

Q7ZYW4

SI:dZ194E12.8 (Novel MHCII alpha chain protein) (Fragment) {GENE:Name=SI:dZ194E12.8} - Brachydanio rerio (Zebrafish) (Danio rerio)

Q7ZYW5

SI:dZ194E12.7 (Novel MHCII beta chain protein) (Fragment) {GENE:Name=SI:dZ194E12.7} - Brachydanio rerio (Zebrafish) (Danio rerio)

Q801W0

SI:dZ266F07.2 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ266F07.2} - Brachydanio rerio (Zebrafish) (Danio rerio)

Q9TPE3

MHC class II antigen (Fragment) {GENE:Name=MhcII} - Polypterus sp. (Bichir)

Q9TPE4

MHC class II antigen (Fragment) {GENE:Name=MhcII} - Polypterus sp. (Bichir)

in Swiss-Prot/TrEMBL by AC, ID, description,
gene name, organism

**Please do NOT use any boolean operators (and,
or, etc.)**


If you would like to retrieve all the Swiss-Prot/TrEMBL entries contained in this list , you can enter a file name. These entries will then be saved to a file under this name in the directory outgoing of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ☒ Swiss-Prot ☐ Fasta

or

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)[Hosted by NCSC US](#)[Mirror sites:](#)[Australia](#)[Bolivia](#)[Canada](#)[China](#)[Korea](#)[Switzerland](#)[Taiwan](#)

 Expasy Home page	Site Map	Search Expasy	Contact us	Swiss-Prot
<div>Hosted by NCSC US</div> <div>Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan</div>				
Search <input type="text" value="Swiss-Prot/TrEMBL"/> <input type="button" value="Go"/> for <input type="text" value="mhci"/> <input type="button" value="Clear"/>				

Search in Swiss-Prot and TrEMBL for: mhci

Swiss-Prot Release 44.2 of 30-Jul-2004

TrEMBL Release 27.2 of 30-Jul-2004

- Number of sequences found in [Swiss-Prot](#)₍₀₎ and [TrEMBL](#)₍₇₎: 7
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the [bottom](#) of this page.
- For more directed searches, you can use the Sequence Retrieval System [SRS](#).

Search in Swiss-Prot: There are matches to 0 out of 155596 entries

Search in TrEMBL: There are matches to 7 out of 1365262 entries

[Q7ZYYW1](#)

SI:dZ194E12.12 (Novel MHCII beta chain protein) (Fragment) {GENE:Name=SI:dZ194E12.12} - Brachydanio rerio (Zebrafish)
(Danio rerio)

[Q7ZYYW2](#)

SI:dZ194E12.11 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ194E12.11} - Brachydanio rerio (Zebrafish) (Danio rerio)

[Q7ZYYW4](#)

SI:dZ194E12.8 (Novel MHCII alpha chain protein) (Fragment) {GENE:Name=SI:dZ194E12.8} - Brachydanio rerio (Zebrafish) (Danio rerio)

[Q7ZYYW5](#)

SI:dZ194E12.7 (Novel MHCII beta chain protein) (Fragment) {GENE:Name=SI:dZ194E12.7} - Brachydanio rerio (Zebrafish) (Danio rerio)
Q801W0
SI:dZ266F07.2 (Novel MHCII alpha chain protein) {GENE:Name=SI:dZ266F07.2} - Brachydanio rerio (Zebrafish) (Danio rerio)
Q9TPE3
MHC class II antigen (Fragment) {GENE:Name=MhclI} - Polypterus sp. (Bichir)
Q9TPE4
MHC class II antigen (Fragment) {GENE:Name=MhclI} - Polypterus sp. (Bichir)

[New Search](#)

in Swiss-Prot/TrEMBL by AC, ID, description, gene name, organism
Please do NOT use any boolean operators (and, or, etc.)

If you would like to retrieve all the Swiss-Prot/TrEMBL entries contained in this list, you can enter a file name. These entries will then be saved to a file under this name in the directory outgoing of the [ExpASY](#) anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ☒ Swiss-Prot ☐ Fasta

[Reset](#)[or](#) [Create file](#)

 ExpASY Home page	Site Map	Search ExpASY	Contact us	Swiss-Prot
Hosted by NCSC US Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan				

Search for

NiceProt View of Swiss-Prot: Q53654

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name **CNA_STAAU**
 Primary accession number **Q53654**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 37, December 1998
 Sequence was last modified in Release 37, December 1998
 Annotations were last modified in Release 45, October 2004

Name and origin of the protein

Protein name **Collagen adhesin [Precursor]**
 Synonyms None
 Gene name **Name: cna**
 From **Staphylococcus aureus [TaxID: 1280]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=FDA 574;
 MEDLINE=92165839;PubMed=1311320 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Patti J.M.](#), [Jonsson H.](#), [Guss B.](#), [Switalski L.M.](#), [Wiberg K.](#), [Lindberg M.](#), [Hoeoek M.](#);
 "Molecular characterization and expression of a gene encoding a Staphylococcus aureus collagen adhesin."; [J. Biol. Chem. 267:4766-4772\(1992\)](#).
 [2] ERRATUM.
[Patti J.M.](#), [Jonsson H.](#), [Guss B.](#), [Switalski L.M.](#), [Wiberg K.](#), [Lindberg M.](#), [Hoeoek M.](#);
[J. Biol. Chem. 269:11672-11672\(1994\)](#).

[Printer-friendly view](#) [Submit update](#) [Quick BlastP search](#)

[3] COLLAGEN-BINDING DOMAIN.

STRAIN=FDA 574;

MEDLINE=94032261;PubMed=8218209 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]

Patti J.M., Boles J.O., Hoeoek M.;

"Identification and biochemical characterization of the ligand binding domain of the collagen adhesin from *Staphylococcus aureus*."; Biochemistry 32:11428-11435(1993).

[4] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.

MEDLINE=97475225;PubMed=9334749 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]

Symersky J., Patti J.M., Carson M., House-Pompeo K., Teale M., Moore D., Jin L., Schneider A., DeLucas L.J., Hoeoek M., Narayana S.V.L.;

"Structure of the collagen-binding domain from a *Staphylococcus aureus* adhesin. ";

Nat. Struct. Biol. 4:833-838(1997).

Comments

- **FUNCTION**: Mediates attachment of staphyococcal cells to collagen-containing substrata.
- **SUBCELLULAR LOCATION**: Attached to the cell wall peptidoglycan by an amide bond (*Potential*).

Copyright

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch)

Cross-references

EMBL

M81736; AAA20874.1; -[[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

1AMX; 24-JUN-98.[[ExpASY](#) / [RCSB](#) / [EBI](#)]

1D2O; 27-SEP-00. [[ExpASY](#) / [RCSB](#) / [EBI](#)]

1D2P; 27-SEP-00. [[ExpASY](#) / [RCSB](#) / [EBI](#)]

[Detailed list of linked structures.](#)

[IPR008966](#); Adhes_bact.

[IPR008454](#); Cna_B.

[IPR008970](#); Cna_B_unit.

[IPR008456](#); Collagen_bind.

[IPR001899](#); Gram_pos_anchor.

[Graphical view of domain structure.](#)

[PF05738](#); Cna_B; 7.

[PF05737](#); Collagen_bind; 1.

[Pfam](#) graphical view of domain structure.

[TIGR01167](#); LPXTG_anchor; 1.

TIGRFAMs

[PS50847](#); GRAM_POS_ANCHORING; FALSE_NEG.

PROSITE graphical view of domain structure.

[Domain structure / List of seq. sharing at least 1 domain]

[Family / Alignment / Tree]

Q53654.

Q53654.

053654.

Q53654.

053654.

053654.

O53654: B6A1CC072E575D76.

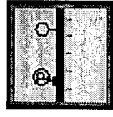
Get region on 2D PAGE.

View cluster of proteins with at least 50% / 90% identity.

Keywords

3D-structure; Cell wall; Peptidoglycan-anchor; Repeat; Signal.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	<u>1</u>	<u>29</u>	29	Potential.
CHAIN	<u>30</u>	<u>1154</u>	1125	Collagen adhesin.
PROPEP	<u>1155</u>	<u>1183</u>	29	Removed by sortase (Potential).
DOMAIN	<u>151</u>	<u>318</u>	168	Collagen-binding.
DOMAIN	<u>533</u>	<u>1093</u>	561	3 X 187 AA approximate tandem repeats.
DOMAIN	<u>1093</u>	<u>1157</u>	65	Lys/Pro-rich; cell wall-spanning.
REPEAT	<u>533</u>	<u>719</u>	187	B1.
REPEAT	<u>720</u>	<u>906</u>	187	B2.
REPEAT	<u>907</u>	<u>1093</u>	187	B3.
SITE	<u>1151</u>	<u>1155</u>	5	LPXTG sorting signal (Potential).
MOD_RES	<u>1154</u>	<u>1154</u>		Pentaglycyl murein peptidoglycan amidated threonine (Potential).
STRAND	<u>174</u>	<u>179</u>	6	
TURN	<u>182</u>	<u>183</u>	2	
TURN	<u>185</u>	<u>186</u>	2	

STRAND	<u>187</u>	<u>194</u>	8
TURN	<u>196</u>	<u>197</u>	2
STRAND	<u>201</u>	<u>201</u>	1
STRAND	<u>205</u>	<u>211</u>	7
STRAND	<u>215</u>	<u>228</u>	14
TURN	<u>229</u>	<u>230</u>	2
STRAND	<u>232</u>	<u>234</u>	3
HELIX	<u>239</u>	<u>246</u>	8
TURN	<u>248</u>	<u>249</u>	2
STRAND	<u>251</u>	<u>255</u>	5
TURN	<u>256</u>	<u>259</u>	4
STRAND	<u>260</u>	<u>265</u>	6
HELIX	<u>267</u>	<u>270</u>	4
TURN	<u>271</u>	<u>272</u>	2
STRAND	<u>273</u>	<u>283</u>	11
TURN	<u>286</u>	<u>287</u>	2
STRAND	<u>290</u>	<u>299</u>	10
STRAND	<u>301</u>	<u>301</u>	1
TURN	<u>302</u>	<u>303</u>	2
STRAND	<u>307</u>	<u>311</u>	5
STRAND	<u>314</u>	<u>317</u>	4
STRAND	<u>534</u>	<u>544</u>	11
TURN	<u>546</u>	<u>550</u>	5
STRAND	<u>556</u>	<u>563</u>	8
TURN	<u>564</u>	<u>565</u>	2
STRAND	<u>566</u>	<u>574</u>	9
HELIX	<u>575</u>	<u>577</u>	3
TURN	<u>578</u>	<u>579</u>	2
STRAND	<u>580</u>	<u>587</u>	8
STRAND	<u>589</u>	<u>590</u>	2
TURN	<u>591</u>	<u>592</u>	2
STRAND	<u>593</u>	<u>594</u>	2
STRAND	<u>597</u>	<u>601</u>	5
TURN	<u>605</u>	<u>606</u>	2
STRAND	<u>607</u>	<u>612</u>	6

TURN	613	614	2
STRAND	615	620	6
TURN	622	623	2
STRAND	624	634	11
TURN	636	640	5
STRAND	646	653	8
TURN	654	655	2
STRAND	656	665	10
HELIX	666	668	3
TURN	669	670	2
STRAND	671	678	8
STRAND	680	680	1
STRAND	685	685	1
STRAND	688	692	5
TURN	697	698	2
STRAND	700	704	5
TURN	708	709	2
STRAND	711	716	6
STRAND	721	731	11
TURN	733	737	5
STRAND	744	750	7
TURN	751	752	2
STRAND	753	760	8
HELIX	762	764	3
TURN	765	765	1
STRAND	767	774	8
STRAND	776	777	2
TURN	778	779	2
STRAND	780	781	2
STRAND	784	788	5
TURN	792	793	2
STRAND	794	799	6
TURN	800	801	2
STRAND	802	807	6
TURN	809	810	2

Search

Swiss-Prot/TrEMBL

▼

for

cna staphylococcus

Go

Clear

NiceProt View of

TrEMBL: Q6GDB2

Entry info

Name and origin

References

Comments

Cross-references

Keywords

Features

Sequence

Tools

Printer-friendly view

Request update

Quick BlastP search

Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name	Q6GDB2
Primary accession number	Q6GDB2
Secondary accession numbers	None
Entered in TrEMBL in	Release 28, October 2004
Sequence was last modified in	Release 28, October 2004
Annotations were last modified in	Release 28, October 2004

Name and origin of the protein

Protein name	Collagen adhesin
Synonyms	None
Gene name	Name: cna
	ORFNames: SAR2774

From [Staphylococcus aureus subsp. aureus MRSA252](#) [TaxID: 282458]

Taxonomy [Bacteria](#); [Firmicutes](#); [Bacillales](#); [Staphylococcus](#).

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=MRSA252;

[Holden M.T.G.](#), [Feil E.J.](#), [Lindsay J.A.](#), [Peacock S.J.](#), [Day N.P.J.](#), [Enright M.C.](#), [Foster T.J.](#), [Moore C.E.](#), [Hurst L.](#), [Atkin R.](#), [Barron A.](#), [Bason N.](#), [Bentley S.D.](#), [Chillingworth C.](#), [Chillingworth T.](#), [Churcher C.](#), [Clark L.](#), [Corton C.](#), [Cronin A.](#), [Doggett J.](#), [Dowd L.](#), [Feltwell T.](#), [Hance Z.](#), [Harris B.](#), [Hauser H.](#), [Holroyd S.](#), [Jagels K.](#), [James K.D.](#), [Lennard N.](#), [Line A.](#), [Mayes R.](#), [Moule S.](#), [Mungall K.](#), [Ormond D.](#), [Quail M.A.](#), [Rabbinowitsch E.](#), [Rutherford K.](#), [Sanders M.](#), [Sharp S.](#), [Simmonds M.](#), [Stevens K.](#), [Whitehead S.](#), [Barrell B.G.](#), [Spratt B.G.](#), [Parkhill J.](#);

"Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance."; [Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791\(2004\)](#).

STRAND	<u>811</u>	<u>821</u>	11
HELIX	<u>823</u>	<u>825</u>	3
TURN	<u>826</u>	<u>827</u>	2
STRAND	<u>833</u>	<u>840</u>	8
TURN	<u>841</u>	<u>842</u>	2
STRAND	<u>843</u>	<u>852</u>	10
TURN	<u>853</u>	<u>857</u>	5
STRAND	<u>858</u>	<u>865</u>	8
STRAND	<u>867</u>	<u>868</u>	2
TURN	<u>869</u>	<u>870</u>	2
STRAND	<u>871</u>	<u>872</u>	2
STRAND	<u>875</u>	<u>879</u>	5
TURN	<u>884</u>	<u>885</u>	2
STRAND	<u>886</u>	<u>891</u>	6
HELIX	<u>895</u>	<u>897</u>	3
STRAND	<u>898</u>	<u>904</u>	7

Sequence information

Length: 1183 AA [This is the length of the unprocessed precursor]

Molecular weight: 133066 Da [This is the MW of the unprocessed precursor]

CRC64: B6A1CC072E575D76 [This is a checksum on the sequence]

10	20	30	40	50	60
MNKNVLKFMV	FIMLLNIITP	LFNKNEAFAA	RDISSTNVTD	LTVSPSKIED	GGKTTVKMTF
70	80	90	100	110	120
DDKNGKIQNG	DMIKVAVPTS	GTVKIEGYSK	TVPLTVKGEQ	VGQAVITPDG	ATITFNDKVE
130	140	150	160	170	180
KLSDVSGFAE	FEVQGRNLTQ	TNTSDDKVAT	ITSGNKSTNV	TVHKSEAGTS	SVFYKYKTGDM
190	200	210	220	230	240
LPEDTTHVRW	FLNINNEKSY	VSKDITIKDQ	IQGGQQLDLS	TLNINVTGTH	SNYYSGQSAI
250	260	270	280	290	300
TDFEKAFPGS	KITVDNTKNT	IDVTIPQGYG	SYNSFSINYK	TKITNEQQKE	FVNNSQAWYQ

310		320		330		340		350		360
EHGKEEVNGK	SNHHTVHNIN	ANAGIEGTVK	GELKVLKQDK	DTKAPIANVK	FKLSKKDGSV					
370		380		390		400		410		420
VKDNQKEIEI	ITDANGIANI	KALPSGDYIL	KEIEAPRPYT	FDKDKKEYPFT	MKDTDNQGYF					
430		440		450		460		470		480
TTIENAKAIE	KTKDVSQAQV	WEGTQKVKPT	IYFKLYKQDD	NQNTTPVDKA	EIKKLEDGTT					
490		500		510		520		530		540
KVTWSNLPEN	DKNGKAIKYL	VKEVNAQGED	TTPEGYTKKE	NGLVVTNTEK	PIETTTSISGE					
550		560		570		580		590		600
KWDDDKDNQD	GKRPEKVSVN	LLANGEKVKT	LDVTSETNWK	YEFKDLPKYD	EGKKIEYTVT					
610		620		630		640		650		660
EDHVKDYTTD	INGTTITNKY	TPGETSATVT	KNWDDNNNQD	GKRPTTEIKVE	LYQDGKATGK					
670		680		690		700		710		720
TAILNESNNW	THTWTGLDEK	AKGQQVKYTV	EELTKVKGYT	THVDNNDMGN	LIVTNKYTPE					
730		740		750		760		770		780
TTSISGEKW	DDKDNQDGKR	PEKVSVNLLA	DGEKVKTLDV	TSETNWKYEF	KDLPKYDEGK					
790		800		810		820		830		840
KIEYTVTEDH	VKDYTTDDING	TTITNKYTPG	ETSATVTKNW	DDNNNQDGKR	PTEIKVELYQ					
850		860		870		880		890		900
DGKATGKTAI	LNESNNWTHT	WTGLDEKAKG	QQVKYTVVEEL	TKVKGYTTHV	DNNDMGNLIV					
910		920		930		940		950		960
TNKYTPETTS	ISGEKWDDDK	DNQDGKRPEK	VSVNLLANGE	KVKTLDDVTSE	TNWKYEFKDL					

970 980 990 1000 1010 1020
PKYDEGKKIE YTVTEDHVKD YTTDINGTTI TNKYTPGETS ATVTKNWDDN NNQDGKRPTE
1030 1040 1050 1060 1070 1080
IKVELYQDGK ATGKTAILNE SNNWTHWTG LDEKAKGQQV KYTVDELTKV NGYTTTHVDNN
1090 1100 1110 1120 1130 1140
DMGNLIVTNK YTPKKPNKPI YPEKPKDKTP PTKPDHSNKV KPTPPDKPSK VDKDDQPKDN
1150 1160 1170 1180
KTKPENPLKE LPKTGMKIIT SWITWVFIGI LGLYLILRKR FNS

Q53654 in [FASTA format](#)

[View entry in original Swiss-Prot format](#)
[View entry in raw text format \(no links\)](#)
[Report form for errors/updates in this Swiss-Prot entry](#)

BLAST [BLAST submission on ExpASY/SIB](#)
or at [NCBI \(USA\)](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),
[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



Search the [SWISS-MODEL Repository](#)

ExpASY Home page	Site Map	Search ExpASy	Contact us	Swiss-Prot
Hosted by NCSC US Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan				

None

Cross-references

EMBL BX571856; CAG41749.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
ProDom [Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN [Family / Alignment / Tree]
ProtoMap Q6GDB2.
PRESAGE Q6GDB2.
ModBase Q6GDB2.
SMR Q6GDB2; 24FB7F7244D42C34.
SWISS-2DPAGE Get region on 2D PAGE.
UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Collagen.

Features

None

Sequence information

Length: 1183 AA Molecular weight: 133048 Da CRC64: 24FB7F7244D42C34 [This is a checksum on the sequence]

10		20		30		40		50		60	
MNKNVLKFMV	FIMLLNIITP	LFNKNEAFAA	RDISSTNVTD	LTVSPSKIED	GGKTTVKMTF						
70		80		90		100		110		120	
DDKNGKIQNG	DTIKVAVPTS	GTVKIEGYSK	TVSLTVKGEQ	VGQAVITPDG	ATITFNDKVE						
130		140		150		160		170		180	
KLSDVSGFAE	FEVQGRNLTQ	TNTSDDKVAT	ITSGNKSTNV	TVHKSEAGTS	SVFYFKTGDM						
190		200		210		220		230		240	
LPEDTTHVRW	FLNINNEKRY	VSKDITIKDQ	IQQGQQLDLS	TLNINVTGTH	SNYYSGPNAI						
250		260		270		280		290		300	
TDFEKAFPGS	KITVDNTKNT	IDVTIPQGYG	SLNSFSINYK	TKITNEQQKE	FVNNSQAWYQ						

310		320		330		340		350		360	
EHGKEEVNGK	AFNHTVHNIN	ANAGIEGTVK	GELKVLKQDK	DTKAPIANVK	FKLSKKDGSV						
370		380		390		400		410		420	
VKDNQKEIEI	KTDANGIANI	KALPSGDYIL	KEIEAPAPYT	FDKKEYPFT	MKDTDNQGYF						
430		440		450		460		470		480	
TTIENAKEIE	KTKDVSAQKV	WEGTQVKVPT	IYFKLYKQDD	NQNTTPVDKA	EIKKLEDGTT						
490		500		510		520		530		540	
KVTWSNLPEN	DNKGKTIKYL	VKEVNAQGKD	TTPEGYTKKE	DGLVVTNTEK	PIETTSISGE						
550		560		570		580		590		600	
KVWDDKDNQD	GKRPEKVSVN	LLANGEKVET	VDVTSETNWK	YKFKDLPKYD	EGKKIEYTVT						
610		620		630		640		650		660	
EDHVKDYTTD	INGTTITNKY	TPGETSATVT	KNWDDNNNQD	GKRPTKIVE	LYQDGKATGK						
670		680		690		700		710		720	
TATLINESNNW	THTWTGLDEK	AKGQQVKYTV	EELTKVKGYT	THVDNNDMGN	LIVTNKYTPE						
730		740		750		760		770		780	
TTSISGEKVW	DDKNQDGKR	PEKVSVNLLA	NGEKVKTLDV	TSETNWKYEF	KDLPKYDEGK						
790		800		810		820		830		840	
KIEYTVTEDH	VKDYTTDING	TTITNKYTPG	ETSATVTKNW	DDNNNQDGKR	PTEIKVELYQ						
850		860		870		880		890		900	
DGKATVKTAT	LNESNNWTHT	WTGLDEKAKG	QQVKYTVVEEL	TKVKGYTTHV	DNNDMGNLIV						
910		920		930		940		950		960	
TNKYTPETTS	ISGEKVWDDK	DNQDGKRPEK	VSVNLLANGE	KVKTLDDVTSE	TNWKYEFKNL						

970 | 980 990 1000 1010 1020
PKYDEGKKIE YTVTEDHVKD YTTDINGTTI TNKYTPGETS ATVTKNWDDN NNQDGKRPTIE
1030 | 1040 1050 1060 1070 1080
IKVELYQDGK ATGKTATLNE SNNWTHWTG LDEKAKGQQV KYTVEELTKV NGYTTHVDNN
1090 | 1100 1110 1120 1130 1140
DMGNLIVTNK YTPEKPNKPI YPEKPKDKTP PTKPDHSNKV KPTPPDKPSK VDKDDQPKDN
1150 | 1160 1170 1180
KTKPENPLKE LPKTGMKIIT SWITWVFIGI LGLYLILRKR FNS

Q6GDB2 in [FASTA format](#)

[View entry in original TrEMBL format](#)
[View entry in raw text format \(no links\)](#)
[Request for annotation of this TrEMBL entry](#)



[ScanProsite](#), [MotifScan](#)

BLAST [BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),
[PeptideMass](#), [PeptideCutter](#), [Dotlet](#) (Java)



Search the [SWISS-MODEL Repository](#)

ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Hosted by NCSC US	Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan			

NiceProt View of TrEMBL: Q53630

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **Q53630**
 Primary accession number **Q53630**
 Secondary accession numbers None
 Entered in TrEMBL in Release 01, November 1996
 Sequence was last modified in Release 18, October 2001
 Annotations were last modified in Release 24, June 2003

Name and origin of the protein

Protein name **Cell surface elastin binding protein**
 Synonyms None
 Gene name **Name: ebpS**
 From **Staphylococcus aureus [TaxID: 1280]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 12598;
 MEDLINE=96279109;PubMed=8663124 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
 Park P.W., Rosenbloom J., Abrams W.R., Rosenbloom J., Mecham R.P.;
 "Molecular cloning and expression of the gene for elastin-binding protein (ebpS) in *Staphylococcus aureus*."; *J. Biol. Chem.* 271:15803-15809(1996).
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 12598;
 MEDLINE=21634882;PubMed=11684686 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

Downer R., Roche F., Park P.W., Mecham R.P., Foster T.J.;

"The elastin-binding protein of Staphylococcus aureus (EbpS) is expressed at the cell surface as an integral membrane protein and not as a cell-wall associated protein.";

J. Biol. Chem. 277:243-250(2002).

[3] SEQUENCE FROM NUCLEIC ACID.

STRAIN=ATCC 12598;

Roche F.M., Foster T.J.;

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

Comments

None

Cross-references

EMBL

U48826; AAC44135.2; -.[\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)

GO

[GO:0016998](#); Biological process: cell wall catabolism (*inferred from electronic annotation*).

InterPro

[IPR002482](#); LysM.

[Graphical view of domain structure](#).

Pfam

[PF01476](#); LysM; 1.

[Pfam graphical view of domain structure](#).

SMART

[SM00257](#); LysM; 1.

ProDom

[\[Domain structure / List of seq. sharing at least 1 domain\]](#)

HOBACGEN

[\[Family / Alignment / Tree\]](#)

ProtoMap

[Q53630](#).

PRESAGE

[Q53630](#).

ModBase

[Q53630](#).

SMR

[Q53630](#); 62904CF86C1F56B8.

SWISS-2DPAGE

[Get region on 2D PAGE](#).

UniRef

[View cluster of proteins with at least 50% / 90% identity](#).

Keywords

None

Features

None

Sequence information

Length: **486 AA** Molecular weight: **53080 Da** **CRC64: 62904CF86C1F56B8** [This is a checksum on the sequence]

10	20	30	40	50	60
----	----	----	----	----	----

<http://us.expasy.org/cgi-bin/niceprot.pl?Q53630>

8/4/04

MSNNFKDDFE	KNRQSIDTNS	HQDHTEDVEK	DQSELEHQDT	IENTEQQFPP	RNAQRRKRRR
70	80	90	100	110	120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	QVESHSHSTE	SQEPHQDST	PQHEEGYYNK
130	140	150	160	170	180
NAFAMDKSHP	EPIEDNDKHE	TIKEAENNTE	HSTVSDKSEA	EQSQQPKPYF	ATGANQANTS
190	200	210	220	230	240
KDKHDDVTVK	QDKDESKDHH	SGKKGAAIGA	GTAGVAGAAG	AMGVSKAKKH	SNDAQNKSNS
250	260	270	280	290	300
GKVNNSTEDK	ASEDKSKEHH	NGKKGAAIGA	GTAGLAGGAA	SNSASAASKP	HASNNASQNN
310	320	330	340	350	360
DEHDHHRDK	ERKKGGMAKV	LLPLIAAVLI	IGALAIFGGM	ALNNHNNGTK	ENKIAINTNKN
370	380	390	400	410	420
NADESKDKDT	SKDASKDKSK	STDSDKSKDD	QDKATKDESD	NDQNNANQAN	NQAQNNQNQQ
430	440	450	460	470	480
QANQNQQQQQ	QRQGGGQRHT	VNGQENLYRI	AIQYYGSGSP	ENVEKIRRAN	GLSGNNIRNG

QQIVIP

Q53630 in FASTA format

[View entry in original TrEMBL format](#)
[View entry in raw text format \(no links\)](#)
[Request for annotation of this TrEMBL entry](#)

BLAST submission on ExPASy/SIB

Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),

BLAST
or at [NCBI \(USA\)](#)

[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



Search the [SWISS-MODEL Repository](#)



 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Hosted by NCSC US	Mirror sites: Australia Bolivia Canada China Korea Switzerland Taiwan			

Search for

NiceProt View of TrEMBL: Q6GGT1

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the [user manual](#) or [other documents](#).

Entry information

Entry name **Q6GGT1**
 Primary accession number **Q6GGT1**
 Secondary accession numbers None
 Entered in TrEMBL in Release 28, October 2004
 Sequence was last modified in Release 28, October 2004
 Annotations were last modified in Release 28, October 2004

Name and origin of the protein

Protein name **Cell surface elastin binding protein**
 Synonyms None

Gene name **Name: ebpS**
 ORFNames: SAR1489
 From **Staphylococcus aureus subsp. aureus MRSA252 [TaxID: 282458]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=MRSA252;

Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M., Sharp S., Simmons M., Stevens K., Whitehead S., Barrell B.G., Pratt B.G., Parkhill J.;

"Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance.";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

None

Cross-references

EMBL BX571856; CAG40487.1; -[[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

ProDom [Domain structure / List of seq. sharing at least 1 domain]

HOBACGEN [[Family](#) / [Alignment](#) / [Tree](#)]

ProtoMap [Q6GGT1](#).

PRESAGE [Q6GGT1](#).

ModBase [Q6GGT1](#).

SMR [Q6GGT1](#); 62904CF86C1F56B8.

SWISS-2DPAGE [Get region on 2D PAGE](#).

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features

None

Sequence information

Length: 486 AA Molecular weight: 53080 Da CRC64: 62904CF86C1F56B8 [This is a checksum on the sequence]

10		20		30		40		50		60
MSNNFKDDFE	KNRQSIDTNS	HQDHTEDVEK	DQSELEHQDT	IENTEQQFPP	RNAQRRKRRR					
70		80		90		100		110		120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	RQVESSHSTE	SQEPSHQDST	PQHEEGYYNK					
130		140		150		160		170		180
NAFAMDKSHP	EPIEDNDKHE	TIKEAENNTE	HSTVSDKSEA	EQSQQPKPYF	ATGANQANTS					
190		200		210		220		230		240
KDKHDDVTVK	QDKDESKDHH	SGKKGAAIGA	GTAGVAGAAG	AMGVSKAKKH	SNDAQNKSNS					
250		260		270		280		290		300
GKVNNSTEDK	ASEDKSKEHH	NGKKGAAIGA	GTAGLAGGAA	SNSASAASKP	HASNNASQNN					

310	320	330	340	350	360
DEHDHHRDK	ERKKGMAKV	LLPLIAAVLI	IGALAIFGGM	ALNNHNGTK	ENKIANTNKN
370	380	390	400	410	420
NADESKDKDT	SKDASKDKSK	STSDSKSKDD	QDKATKDESD	NDQNNANQAN	NQAQNNQNQQ
430	440	450	460	470	480
QANQNQQQQQ	QRQGGQRHT	VNGQENLYRI	AIQYYGSGSP	ENVEKIRRAN	GLSGNNIRNG

QQIVIP

Q6GGT1 in FASTA format

[View entry in original TrEMBL format](#)
[View entry in raw text format \(no links\)](#)
[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)



[ScanProsite](#), [MotifScan](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),
[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



Search the [SWISS-MODEL Repository](#)

ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
<div> Hosted by NCSC US </div> <div> Mirror sites: <div> Australia </div> <div> Bolivia </div> <div> Canada </div> <div> China </div> <div> Korea </div> <div> Switzerland </div> <div> Taiwan </div> </div>				

NiceProt View of TrEMBL: Q7A5I6

[\[Entry info\]](#)
[\[Name and origin\]](#)
[\[References\]](#)
[\[Comments\]](#)
[\[Cross-references\]](#)
[\[Keywords\]](#)
[\[Features\]](#)
[\[Sequence\]](#)
[\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **Q7A5I6**
 Primary accession number **Q7A5I6**
 Secondary accession numbers None
 Entered in TrEMBL in Release 27, July 2004
 Sequence was last modified in Release 27, July 2004
 Annotations were last modified in Release 27, July 2004

Name and origin of the protein

Protein name **Elastin binding protein**
 Synonyms None
 Gene name **Name: ebpS**
 From **Staphylococcus aureus (strain N315) [TaxID: 158879]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=N315;

[Kuroda M.](#), [Ohta T.](#), [Uchiyama I.](#), [Baba T.](#), [Yuzawa H.](#), [Kobayashi I.](#), [Cui L.](#), [Oguchi A.](#), [Aoki K.](#), [Nagai Y.](#), [Lian J.](#), [Ito T.](#), [Kanamori M.](#), [Matsumaru H.](#), [Maruyama A.](#), [Murakami H.](#), [Hosoyama A.](#), [Mizutani-Ui Y.](#), [Takahashi N.K.](#), [Sawano T.](#), [Inoue R.](#), [Kaio C.](#), [Sekimizu K.](#), [Hirakawa H.](#), [Kuhara S.](#), [Goto S.](#), [Yabuzaki J.](#), [Kanehisa M.](#), [Yamashita A.](#), [Oshima K.](#), [Furuya K.](#), [Yoshino C.](#), [Shiba T.](#), [Hattori M.](#), [Ogasawara N.](#), [Hayashi H.](#), [Hiramatsu K.](#);

"Whole genome sequencing of meticillin-resistant Staphylococcus aureus."
 Lancet 357:1225-1240(2001).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=N315;
Director-General, [Biotechnology Center](#), [Aoki K.](#), [Oguchi A.](#), [Hosoyama A.](#), [Nagai Y.](#), [Kuroda M.](#), [Hiramatsu K.](#), [Kikuchi H.](#);
Submitted (JAN-2001) to the [EMBL/GenBank/DBJ](#) databases.

Comments

None

Cross-references

EMBL [AP003134](#); [BAB42574.1](#); -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
ProDom [[Domain structure](#) / [List of seq. sharing at least 1 domain](#)]
HOBACGEN [[Family](#) / [Alignment](#) / [Tree](#)]
ProtoMap [Q7A5I6](#).
PRESAGE [Q7A5I6](#).
ModBase [Q7A5I6](#).
SMR [Q7A5I6](#); [F4DA049456C09A36](#).
SWISS-2DPAGE [Get region on 2D PAGE](#).
UniRef [View cluster of proteins with at least 50% / 90% identity](#).

Keywords

None

Features

None

Sequence information

Length: 486 AA Molecular weight: 53181 Da CRC64: [F4DA049456C09A36](#) [This is a checksum on the sequence]

10	20	30	40	50	60
MSNNFKDDFE	KNRQSIDTNS	HQDHTEDVEK	DQSELEHQDT	IENTEQQFPP	RNAQRRKRRR
70	80	90	100	110	120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	RQVESSHSTE	SQEPSHQDST	PQHEEEYYNK
130	140	150	160	170	180
NAFAMDKSHP	EPIEDNDKHE	TIKDAENNTE	HSTVSDKSIA	EQSQQPKPYF	ATGANQANTS
190	200	210	220	230	240
KDKHDDVTVK	QDKDESKDHH	SGKKGAAIGA	GTAGVAGAAG	AMGVSKAKKH	SNDAQNKSNS

250 | 260 270 280 290 300
DKSNNSTEDK ASQDKSKDHH NGKKGAAIGA GTAGLAGGAA SKSASAASKP HASNNASQNH
310 | 320 330 340 350 360
DEHDNHRDK ERKKGGMKV LLPLIAAVLI IGALAIFGGM ALNNHNNGTK ENKIANTNKN
370 | 380 390 400 410 420
NADESKDKT SKDASKDKSK STSDSKSKED QDKATKDESD NDQNNANQAN NQAQNNQNQQ
430 | 440 450 460 470 480
QANQNQQQQQ QRQGGGQRHT VNGQENLYRI AIQYYGSGSP ENVEKIRРАН GLSGNNIRNG

QQIVIP

Q7A5I6 in FASTA format

[View entry in original TrEMBL format](#)
[View entry in raw text format \(no links\)](#)
[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)

 Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),
[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



Search the [SWISS-MODEL Repository](#)

 <u>ExPASy Home page</u>	<u>Site Map</u>	<u>Search ExPASy</u>	<u>Contact us</u>	<u>Swiss-Prot</u>
Hosted by <u>NCSC.US</u>	Mirror sites: <u>Australia</u> <u>Bolivia</u> <u>Canada</u> <u>China</u> <u>Korea</u> <u>Switzerland</u> <u>Taiwan</u>			

Search for

NiceProt View of

TrEMBL: Q8NWM5

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Printer-friendly view	Request update	Quick BlastP search
---------------------------------------	--------------------------------	-------------------------------------

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **Q8NWM5**
 Primary accession number **Q8NWM5**
 Secondary accession numbers None
 Entered in TrEMBL in Release 22, October 2002
 Sequence was last modified in Release 22, October 2002
 Annotations were last modified in Release 26, March 2004

Name and origin of the protein

Protein name **Elastin binding protein**
 Synonyms None
 Gene name **Name: ebpS**
 From **Staphylococcus aureus (strain MW2) [TaxID: 196620]**
 Taxonomy **Bacteria; Firmicutes; Bacillales; Staphylococcus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=MW2;

MEDLINE=22040717;PubMed=12044378 [NCBI, ExPASy, EBI, Israel, Japan]

[Baba T.](#), [Takeuchi F.](#), [Kuroda M.](#), [Yuzawa H.](#), [Aoki K.-I.](#), [Oguchi A.](#), [Nagai Y.](#), [Iwama N.](#), [Asano K.](#), [Naimi T.](#), [Kuroda H.](#), [Cui L.](#), [Yamamoto K.](#), [Hiramatsu K.](#);

"Genome and virulence determinants of high virulence community-acquired MRSA.";

Lancet 359:1819-1827(2002).

Comments

None

Cross-references

EMBL AP004827; BAB95234.1; -, [EMBL / GenBank / DDBJ] [CoDingSequence]
GO GO:0016998; Biological process: cell wall catabolism (inferred from electronic annotation).
CMR Q8NWM5; Q8NWM5.
InterPro IPR002482; LysM.
Pfam PF01476; LysM; 1.
Pfam graphical view of domain structure.
SMART SM00257; LysM; 1.
ProDom [Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN [Family / Alignment / Tree]
ProtoMap Q8NWM5.
PRESAGE Q8NWM5.
ModBase Q8NWM5.
SMR Q8NWM5; 8859F271713E7218.
SWISS-2DPAGE Get region on 2D PAGE.
UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Complete proteome.

Features

None

Sequence information

Length: 486 AA Molecular weight: 53239 Da CRC64: 8859F271713E7218 [This is a checksum on the sequence]

10	20	30	40	50	60
MSNNFKDDFE	KNRQSIDTNS	HQDHTEDVEK	DQSELEHQDT	IENTEQQFPP	RNAQRRKRRR
70	80	90	100	110	120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	RQVESSHSTE	SQEPSHQDST	PQHEEEYYNK
130	140	150	160	170	180
NAFAMDKSHP	EPIEDNDKHE	TIKEAENNTE	HSTVSDKSEA	EQSQQPKPYF	ATGANQANTS


```

190      |      200      210      220      230      240
KDKHDDVTVK QDKDESKDHH SGKKGAAIGA GTAGVAGAAG AMGVSKAKKH SND AQNKSNS

250      |      260      270      280      290      300
DKSNNSTEDK VSQDKSKDHH NGKKGAAIGA GTAGLAGGAA SKSASAASKP HASNNASQNH

310      |      320      330      340      350      360
DEHDNHRDCK ERKKGGMAKV LLPLIAAVLI IGALAIFGGM ALNNHNNGTK ENK IANTNKN

370      |      380      390      400      410      420
NADESKDKDT SKDASKDKSK STSDSKSKED QDKATKDESD NDQNNANQAN NQAQNNQNQQ

430      |      440      450      460      470      480
QANQNQQQQQ QRQGGGQRHT VNGQENLYRI AIQYYGSGSP ENVEKIRРАН GLSGNNIRNG

```

QQIVIP

Q8NWM5 in [FASTA format](#)

[View entry in original TrEMBL format](#)
[View entry in raw text format \(no links\)](#)
[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)



[ScanProsite](#), [MotifScan](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),
[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



Search the [SWISS-MODEL Repository](#)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Hosted by NCSC US				
Mirror sites:				
Australia				
Bolivia				
Canada				
China				
Korea				
Switzerland				
Taiwan				

NiceProt View of TrEMBL: Q93D59

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **Q93D59**
 Primary accession number **Q93D59**
 Secondary accession numbers None
 Entered in TrEMBL in Release 19, December 2001
 Sequence was last modified in Release 19, December 2001
 Annotations were last modified in Release 24, June 2003

Name and origin of the protein

Protein name **Cell surface elastin binding protein EbpS**
 Synonyms None
 Gene name **Name: ebpS**
 From Staphylococcus aureus [TaxID: 1280]
 Taxonomy Bacteria; Firmicutes; Bacillales; Staphylococcus.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=8325-4;

MEDLINE=21634882;PubMed=11684686 [NCBI, ExPASy, EBL, Israel, Japan]

Downer R., Roche F., Park P.W., Mecham R.P., Foster T.J.;

"The elastin-binding protein of Staphylococcus aureus (EbpS) is expressed at the cell surface as an integral membrane protein and not as a cell-wall associated protein.";

J. Biol. Chem. 277:243-250(2002).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=8325-4;

Roche F.M., Foster T.J.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

Comments

None

Cross-references

EMBL

AF400161; AAL00934.1; -.[[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]

GO

GO:0016998;Biological process: cell wall catabolism (*inferred from electronic annotation*).

InterPro

[IPR002482](#); LysM.

[Graphical view of domain structure](#).

Pfam

[PF01476](#); LysM; 1.

[Pfam graphical view of domain structure](#).

SMART

[SM00257](#); LysM; 1.

ProDom

[\[Domain structure / List of seq. sharing at least 1 domain\]](#)

HOBACGEN

[\[Family / Alignment / Tree\]](#)

ProtoMap

[Q93D59](#).

PRESAGE

[Q93D59](#).

ModBase

[Q93D59](#).

SMR

[Q93D59](#); 70173FD572F47AD8.

SWISS-2DPAGE

[Get region on 2D PAGE](#).

UniRef

[View cluster of proteins with at least 50% / 90% identity](#).

Keywords

None

Features

None

Sequence information

Length: 486 AA Molecular weight: 53221 Da CRC64: 70173FD572F47AD8 [This is a checksum on the sequence]

10	20	30	40	50	60
MSNNFKDDFE	KNRQSIDTNS	HQDHTEDVEK	DQSELEHQDT	IENTEQQFPP	RNAQRRKRRR
70	80	90	100	110	120
DLATNHNKQV	HNESQTSEDN	VQNEAGTIDD	QVVESSHSTE	SQEPHQDST	PQHEEYYNK

130		140	150	160	170	180																																														
NAFAMDKSH	P	E	I	E	D	N	D	K	H	T	I	K	N	A	E	N	N	T	E	H	S	T	V	S	D	K	S	E	A	E	Q	S	Q	Q	P	K	P	Y	F	T	T	G	A	N	Q	S	E	T	S			
190		200	210	220	230	240																																														
KNEHDNDSV	K	Q	D	E	P	K	E	H	H	N	G	K	K	A	A	A	I	G	A	G	T	A	G	V	A	G	A	A	M	A	A	S	K	A	K	K	H	S	N	D	A	Q	N	K	S	N	S					
250		260	270	280	290	300																																														
GKANNSTED	K	A	S	Q	D	K	S	K	D	H	H	N	G	K	K	G	A	A	I	G	A	G	T	A	G	L	A	G	G	A	A	S	K	S	K	S	A	A	A	S	K	P	H	A	S	N	N	A	S	Q	N	H
310		320	330	340	350	360																																														
DEHDNHDRD	K	E	R	K	K	G	M	A	K	V	L	L	P	L	I	A	A	V	L	I	I	G	A	L	A	I	F	G	G	M	A	L	N	N	H	N	G	T	K	E	N	K	I	A	N	T	N	K	N			
370		380	390	400	410	420																																														
NADESKDKT	S	K	D	A	S	K	D	K	S	K	E	D	S	T	D	S	D	K	S	K	E	D	Q	D	K	A	T	K	D	E	S	D	N	Q	N	N	A	N	Q	A	N	Q	N	N	Q	Q						
430		440	450	460	470	480																																														
QANQNQQQQ	Q	Q	R	Q	G	G	Q	R	H	T	V	N	Q	E	N	L	Y	R	I	A	I	Q	Y	Y	G	S	G	S	P	E	N	V	E	K	I	R	R	A	N	G	L	S	G	N	N	I	R	N	G			

QQIVIP

Q93D59 in [FASTA format](#)

[View entry in original TrEMBL format](#)
[View entry in raw text format \(no links\)](#)
[Request for annotation of this TrEMBL entry](#)

BLAST [BLAST submission on ExPASy/SIB](#)
or at [NCBI \(USA\)](#)

 Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#),
[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



Search the [SWISS-MODEL Repository](#)



US 20040101919A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2004/0101919 A1**

Hook et al. (43) **Pub. Date: May 27, 2004**

(54) **BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED PROTEINS FROM GRAM-POSITIVE BACTERIA AND PROTEINS OBTAINED THEREBY**

Related U.S. Application Data

(60) Provisional application No. 60/410,303, filed on Sep. 13, 2002.

Publication Classification

(51) **Int. Cl.⁷** G01N 33/554; G01N 33/569
(52) **U.S. Cl.** 435/7.32

(76) **Inventors:** **Magnus Hook**, Houston, TX (US); **Yi Xu**, Houston, TX (US); **Jouko V. Sillanpaa**, Houston, TX (US); **Narayana Sthanam**, Birmingham, AL (US); **Karthe Ponnuraj**, Birmingham, AL (US); **Joseph M. Patti**, Cumming, GA (US); **Jeff T. Hutchins**, Cumming, GA (US); **Andrea Hall**, Acworth, GA (US); **Maria G. Bowden**, Sugarland, TX (US)

(57) **ABSTRACT**

A bioinformatic method is provided for identifying and isolating proteins with MSCRAMM®-like characteristics from Gram positive bacteria, such as Enterococcus, Staphylococcus, Streptococcus and Bacillus bacteria, which can then be utilized in methods to prevent and treat infections caused by Gram-positive bacteria. The method involves identifying from sequence information those proteins with a putative C-terminal LPXTG (SEQ ID NO:1) cell wall sorting signal and other structural similarities to MSCRAMM® proteins having the LPXTG-anchored cell wall proteins. The MSCRAMM® proteins and immunogenic regions therein that are identified and isolated using the present invention may be used to generate antibodies useful in the diagnosis, treatment or prevention of Gram positive bacterial infections.

Correspondence Address:

STITES & HARBISON PLLC
1199 NORTH FAIRFAX STREET
SUITE 900
ALEXANDRIA, VA 22314 (US)

(21) **Appl. No.: 10/661,809**

(22) **Filed: Sep. 15, 2003**

First Hit

L8: Entry 1 of 22

File: PGPB

Jul 22, 2004

PGPUB-DOCUMENT-NUMBER: 20040142348

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040142348 A1

TITLE: Proteins and polypeptides from coagulase-negative staphylococci

PUBLICATION-DATE: July 22, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
<u>Foster</u> , Timothy J.	Dublin	TX	IE	
McCrea, Kirk	Houston	TX	US	
<u>Hook</u> , Magnus A.O.	Houston	TX	US	
Davis, Stacey	Houston		US	
Nieidhin, Deirdre	Dublin		IE	
Hartford, Orla	Meath		IE	

APPL-NO: 10/ 689082 [PALM]

DATE FILED: October 21, 2003

RELATED-US-APPL-DATA:

Application 10/689082 is a division-of US application 09/386962, filed August 31, 1999, US Patent No. 6635473

Application is a non-provisional-of-provisional application 60/117119, filed January 25, 1999,

Application is a non-provisional-of-provisional application 60/098443, filed August 31, 1998,

INT-CL: [07] C12 Q 1/68, C07 H 21/04, C07 K 14/31

US-CL-PUBLISHED: 435/006; 435/069.1, 435/252.3, 435/320.1, 530/350, 536/023.7

US-CL-CURRENT: 435/6; 435/252.3, 435/320.1, 435/69.1, 530/350, 536/23.7

REPRESENTATIVE-FIGURES: NONE

ABSTRACT:

Proteins and polypeptides from coagulase-negative staphylococcal bacteria such as S. epidermidis, including proteins designated SdrF, SdrG and SdrH, and their effective fragments such as their respective A domains, are provided which are useful in the prevention and treatment of infection caused by coagulase-negative staphylococcal bacteria such as S. epidermidis. The SdrF, SdrG and SdrH proteins are cell-wall associated proteins that specifically bind host proteins and which each have a highly conserved motif of which the consensus sequence is TYTFTDYVD (SEQ ID NO: 16). The proteins and polypeptides may be useful in generating antibodies for the diagnosis and treatment of coagulase-negative staphylococcal infections.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a divisional application of U.S. Appln. Ser. No. 09/386,962, filed Aug. 31, 1999, and claims the benefit of U.S. Provisional Applications Serial No. 60/117,119, filed Jan. 25, 1999, and Serial No. 60/098,443, filed Aug. 31, 1998.